

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2005, 11:38:12 ; Search time 39.7531 Seconds
(without alignments)
169.425 Million cell updates/sec

Title: US-09-743-684A-45

Perfect score: 95

Sequence: 1 XXXXXDVQDXXXXXXXXXXXXX.....XXXXXXXXXXXXXXXXXXXXX 70

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 21350

Minimum DB seq length: 0

Maximum DB seq length: 71

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	25.3	37	2	C41933
2	24	25.3	54	2	H82693
3	24	25.3	56	2	A25507
4	24	25.3	68	2	D82027
5	23	24.2	18	2	B61110
6	23	24.2	43	2	A70231
7	23	24.2	61	2	A20233
8	23	24.2	67	1	TIILF2
9	23	24.2	67	1	TIILF3
10	22	23.2	64	1	TI0AB
11	21	22.1	32	2	S19906
12	21	22.1	35	2	S19909
13	21	22.1	38	2	A60216
14	21	22.1	40	2	T08107
15	21	22.1	40	2	H71330
16	21	22.1	47	2	S23825
17	21	22.1	47	2	I48943
18	21	22.1	51	2	I57670
19	21	22.1	53	2	B25507
20	21	22.1	53	2	T07225
21	21	22.1	53	2	T41761
22	21	22.1	57	2	T03654
23	21	22.1	58	1	Z5BP83
24	21	22.1	63	2	C69303
25	21	22.1	65	2	S05677
26	21	22.1	65	2	H64324
27	21	22.1	66	2	T22505
28	21	22.1	67	1	TI0OC
29	21	22.1	67	2	S33873
30	21	22.1	68	2	F70706
31	21	22.1	69	2	G69004
32	21	22.1	70	2	E83932
33	21	22.1	70	2	T12911
34	21	22.1	71	2	H83014
35	20	21.1	24	2	A05134
36	20	21.1	25	2	S25434
37	20	21.1	28	2	JT0412
38	20	21.1	29	2	AC0717
39	20	21.1	30	2	C32946
40	20	21.1	34	2	B48147
41	20	21.1	36	2	A05135
42	20	21.1	36	2	B82093
43	20	21.1	36	2	H81614
44	20	21.1	37	1	S32792
45	20	21.1	37	2	D69283
46	20	21.1	37	2	S33268
47	20	21.1	40	2	C82780
48	20	21.1	43	2	A61168
49	20	21.1	43	2	A58998
50	20	21.1	44	2	D82579
51	20	21.1	47	2	F83878
52	20	21.1	50	2	T38209
53	20	21.1	50	2	S66218
54	20	21.1	51	2	F90802
55	20	21.1	51	2	PN0457
56	20	21.1	51	2	E85662
57	20	21.1	52	2	G86035
58	20	21.1	53	2	D90189
59	20	21.1	55	2	C29942
60	20	21.1	55	2	D29942
61	20	21.1	56	2	D90257
62	20	21.1	56	2	B29942
63	20	21.1	56	2	A96978
64	20	21.1	58	2	S59072
65	20	21.1	58	2	E81202
66	20	21.1	59	2	E86572
67	20	21.1	59	2	A72052
68	20	21.1	59	2	G95951
69	20	21.1	59	2	AH2461
70	20	21.1	60	2	G81777
71	20	21.1	61	2	AC3158
72	20	21.1	62	1	VDBP22
73	20	21.1	62	2	D81789
74	20	21.1	63	1	RGEERE
75	20	21.1	63	2	A23727
76	20	21.1	64	2	AC0432
77	20	21.1	65	2	A86027
78	20	21.1	66	2	G44196
79	20	21.1	66	2	T44533
80	20	21.1	67	2	T11547
81	20	21.1	68	2	JU0034
82	20	21.1	68	2	E82412
83	20	21.1	68	2	E69536
84	20	21.1	68	2	AC1282
85	20	21.1	68	2	AE3194
86	20	21.1	70	2	B72170
87	20	21.1	70	2	D82529
88	20	21.1	70	2	E72171
89	20	21.1	71	2	F72222
90	19	20.0	13	2	PH1316
91	19	20.0	31	2	E82466
92	19	20.0	33	2	A37479
93	19	20.0	37	2	G82917
94	19	20.0	37	2	B49923
95	19	20.0	37	2	C64219
96	19	20.0	37	2	S62820
97	19	20.0	37	2	A34396
98	19	20.0	38	2	A45588
99	19	20.0	40	2	A59426
100	19	20.0	40	2	D44336

hypothetical prote
ferredoxin 2-oxogl
hypothetical prote
hypothetical prote
50S ribosomal prote
neurotoxin V - sco
gene CPAL leader p
bombyxin-IV chain
hypothetical prote
serine proteinase
troponin I (altern
neurotoxin VIII -
hypothetical prote
hypothetical prote
iberiotoxin - east
conserved hypothet
potassium channel
hypothetical prote
cocoanase (EC 3.4.
epidermal growth f
hypothetical prote
hypothetical prote
probable metalloth
defensin AMPI - Ae
hypothetical prote
basic eosinophil p
hypothetical prote
hypothetical prote
protein translatio
developmental cont
developmental cont
conserved hypothet
developmental cont
zinc finger domain
metallothionein is
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
probable periplasm
hypothetical prote
kil protein - phag
hypothetical prote
regulatory protein
neurotoxin V - bar
hypothetical prote
hypothetical prote
orf7 protein - Mar
hypothetical prote
metallothionein -
long neurotoxin ho
hypothetical prote
hypothetical prote
hypothetical prote
A53L protein - var
hypothetical prote
K8R protein - vari
ribosomal protein
Ig heavy chain DJ
hypothetical prote
huwentoxin-I - Chi
ribosomal protein
ribosomal protein
ribosomal protein
pyrBI leader pep1
kunitz trypsin inh
neurotoxin BmK38 -
neurotoxin Tx3-4 -

ALIGNMENTS

RESULT 1
C41933
mating pheromone Br-20 - Euplotes raikovi
N:Alternate names: euplome
C:Species: Euplotes raikovi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: C41933
R:Raffioni, S.; Miceli, C.; Vallesi, A.; Chowdhury, S.K.; Chait, B.T.; Luporini, P.; Bra
Proc. Natl. Acad. Sci. U.S.A. 89, 2071-2075, 1992
A:Title: Primary structure of Euplotes raikovi pheromones: comparison of five sequences
A:Reference number: A41933; MUID:92196059; PMID:1549567
A:Accession: C41933
A:Molecule type: Protein
A:Residues: 1-37 <RAF>
A:Cross-references: UNIPROT:P26888; PIDN:AAB21809.1; PID:9247247
A:Note: sequence extracted from NCBI backbone (NCBIP:104633)
C:Genetics:
A:Genetic code: SGC9
C:Keywords: pheromone
C:Keywords: bonds: #status predicted
F:3-18,10-32,15-24/Disulfide bonds:
Query Match 25.3%; Score 24; DB 2; Length 37;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 7 DVCQD 11
|:|
Db 1 DICDD 5
RESULT 2
H82693
Hypothetical protein XF1339 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: H82693
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: H82693
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-54 <SIM>
A:Cross-references: UNIPROT:Q9PDP0; GB:AE003966; GB:AE003849; NID:gp106327; PIDN:AAF8414
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Canargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H
de-Neto, E.; Docena, C.; El-Dorri, H.; Facincanli, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1339
Query Match 25.3%; Score 24; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 DVCQD 10
|:|
Db 1 DICDD 5

Db 13 DVCQ 16

RESULT 3
A25507
Proteinase inhibitor (Bowman-Birk) I-2b - wheat (fragment)
C:Species: Triticum aestivum (common wheat)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: A25507
R:Odani, S.; Koide, T.; Ono, T.
J. Biochem. 100, 975-983, 1986
A:Title: Wheat germ trypsin inhibitors. Isolation and structural characterization of sin
A:Reference number: A91908; MUID:87137364; PMID:3818572
A:Accession: A25507
A:Molecule type: protein
A:Residues: 1-56 <ODA>
A:Cross-references: UNIPROT:P09863
C:Superfamily: barley rootlet proteinase inhibitor; Bowman-Birk inhibitor repeat homolog
F:10-35/Domain: Bowman-Birk inhibitor repeat homology <BB1>
Query Match 25.3%; Score 24; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 VCQD 11
|:|
Db 50 VCQD 53
RESULT 4
D82027
Hypothetical protein NMA0318 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: D82027
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:2022556; PMID:10761919
A:Accession: D82027
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-68 <PAR>
A:Cross-references: UNIPROT:Q9JWL2; GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83362
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA0318
Query Match 25.3%; Score 24; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 DVCQ 10
|:|
Db 33 DVCQ 36
RESULT 5
B61110
68k collagen-binding protein, light form - chicken (fragments)
C:Species: Gallus gallus (chicken)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Oct-1994
C:Accession: B61110
R:Tidball, J.G.
J. Biol. Chem. 267, 21211-21219, 1992
A:Title: Identification and distribution of a novel, collagen-binding protein in the dev
A:Reference number: A61110; MUID:93016046; PMID:1328225
A:Accession: B61110
A:Molecule type: Protein
A:Residues: 1-18 <TID>
C:Keywords: collagen binding

Query Match 24.2%; Score 23; DB 2; Length 18;
 Best Local Similarity 80.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 DVCQD 11
 ||||
 Db 1 DVCCLD 5

RESULT 6
 A70231
 C:Species: Borrelia burgdorferi - Lyme disease spirochete plasmid F/lp28-1
 C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
 C:Accession: A70231
 R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White-
 son, D.; Peterson, J.; Kexlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
 Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A:Authors: Smith, H.O.; Venter, J.C.
 A:Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.
 A:Reference number: A70100; MUID:98065943; PMID:9403685
 A:Accession: A70231
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-43 <KLE>
 A:Cross-references: UNIPROT:O51033; GB:AE000794; NID:G2689981; PIDN:AAC66389.1; PID:G269
 A:Experimental source: strain B31
 C:Genetics:
 A:Genome: plasmid

Query Match 24.2%; Score 23; DB 2; Length 43;
 Best Local Similarity 60.0%; Pred. No. 3.5e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 DVCQD 11
 ||||
 Db 20 DMCRD 24

RESULT 7
 AD2033
 hypotheical protein asr1818 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: AD2033
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AD2033
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-61 <KUR>
 A:Cross-references: UNIPROT:Q8YVZ8; GB:BA0000019; PIDN:BA073517.1; PID:G17130908; GSPDB:G
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: asr1818

Query Match 24.2%; Score 23; DB 2; Length 61;
 Best Local Similarity 60.0%; Pred. No. 4.9e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 DVCQD 11
 ||||
 Db 38 DVCCE 42

RESULT 8
 TIILF2
 trypsin inhibitor (Bowman-Birk) II - foxtail millet

C:Species: *Setaria italica* (foxtail millet)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: JX0136
 R:Tashiro, M.; Asao, T.; Hirata, C.; Takahashi, K.; Kanamori, M.
 J. Biochem. 108, 669-672, 1990
 A:Title: The complete amino acid sequence of a major trypsin inhibitor from seeds of fo
 A:Reference number: JX0136; MUID:91154179; PMID:2292595
 A:Accession: JX0136
 A:Molecule type: protein
 A:Residues: 1-67 <TAS>
 A:Cross-references: UNIPROT:P19860
 C:Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
 C:Keywords: duplication; serine proteinase inhibitor
 F:9-34/Domain: Bowman-Birk inhibitor repeat homology <BB1>
 F:35-61/Domain: Bowman-Birk inhibitor repeat homology #status atypical <BB2>
 F:8-63,9-24,14-22,31-38,35-51/Disulfide bonds: #status predicted
 F:16/Inhibitory site: Lys (trypsin) #status predicted

Query Match 24.2%; Score 23; DB 1; Length 67;
 Best Local Similarity 75.0%; Pred. No. 5.3e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 VCQD 11
 ||||
 Db 50 ICQD 53

RESULT 9
 TIILF3
 trypsin inhibitor (Bowman-Birk) III - foxtail millet
 C:Species: *Setaria italica* (foxtail millet)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: JG0013
 R:Tashiro, M.; Asao, T.; Hirata, C.; Takahashi, K.
 Agric. Biol. Chem. 55, 419-426, 1991
 A:Title: Purification, characterization, and amino acid sequence of foxtail millet trypsin
 A:Reference number: JG0013; MUID:91299279; PMID:1368693
 A:Accession: JG0013
 A:Molecule type: protein
 A:Residues: 1-67 <TAS>
 A:Cross-references: UNIPROT:P22737
 C:Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
 C:Keywords: duplication; serine proteinase inhibitor
 F:9-34/Domain: Bowman-Birk inhibitor repeat homology <BB1>
 F:35-61/Domain: Bowman-Birk inhibitor repeat homology #status atypical <BB2>
 F:8-63,9-24,14-22,31-38,35-51/Disulfide bonds: #status predicted
 F:16/Inhibitory site: Lys (trypsin) #status predicted

Query Match 24.2%; Score 23; DB 1; Length 67;
 Best Local Similarity 75.0%; Pred. No. 5.3e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 VCQD 11
 ||||
 Db 50 ICQD 53

RESULT 10
 TIOAB
 trypsin inhibitor (Bowman-Birk) - Job's tears
 C:Species: *Coix lachryma-jobi* (Job's tears)
 C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
 C:Accession: S00349
 R:ARY, M.B.; Shewry, P.R.; Richardson, M.
 FEBS Lett. 229, 111-118, 1988
 A:Title: The amino acid sequence of a cereal Bowman-Birk type trypsin inhibitor from see
 A:Reference number: S00349; MUID:86152203; PMID:3162215
 A:Accession: S00349
 A:Molecule type: protein
 A:Residues: 1-64 <ARY>
 A:Cross-references: UNIPROT:P07679
 C:Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
 C:Keywords: duplication; proteinase inhibitor

F:10-35/Domain: Bowman-Birk inhibitor repeat homology <BB1>
 F:36-59/Domain: Bowman-Birk inhibitor repeat homology #status atypical <BB2>
 F:9-61,10-25,15-23,32-39,36-49/Disulfide bonds: #status predicted
 F:17/Inhibitory site: Arg (trypsin) #status predicted

Query Match 23.2%; Score 22; DB 1; Length 64;
 Best Local Similarity 60.0%; Pred. No. 8e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 DVCQD 11
 | | |
 Db 34 DACKD 38

RESULT 11
 S19906
 E6-II protein - human papillomavirus type 33 (fragment)
 C:Species: human papillomavirus type 33
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: S19906
 R:Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me
 submitted to the EMBL Data Library, January 1992
 A:Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via t
 A:Reference number: S19906
 A:Accession: S19906
 A:Molecule type: mRNA
 A:Residues: 1-32 <SNI>
 A:Cross-references: UNIPROT:081885; EMBL:X64086; NID:g60282; PIDN:CAA45435.1; PID:g60283
 C:Superfamily: papillomavirus E6 protein
 C:Keywords: early protein

Query Match 22.1%; Score 21; DB 2; Length 32;
 Best Local Similarity 75.0%; Pred. No. 6.8e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 DVCQ 10
 | | |
 Db 2 DLQC 5

RESULT 12
 S19909
 E6-III protein - human papillomavirus type 33 (fragment)
 C:Species: human papillomavirus type 33
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: S19909
 R:Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me
 submitted to the EMBL Data Library, January 1992
 A:Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via t
 A:Reference number: S19906
 A:Accession: S19909
 A:Molecule type: mRNA
 A:Residues: 1-35 <SNI>
 A:Cross-references: UNIPROT:081887; EMBL:X64087; NID:g60286; PIDN:CAA45438.1; PID:g60287
 C:Superfamily: papillomavirus E6 protein
 C:Keywords: early protein

Query Match 22.1%; Score 21; DB 2; Length 35;
 Best Local Similarity 75.0%; Pred. No. 7.4e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 DVCQ 10
 | | |
 Db 2 DLQC 5

RESULT 13
 A60216
 hyperglycemic hormone homolog - American lobster (fragments)
 N:Alternate names: peptide G-1
 C:Species: Homarus americanus (American lobster)
 C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 13-Sep-1998
 C:Accession: A60216

R:Pavloff, M.S.; Goy, M.P.
 J. Neurochem. 55, 788-797, 1990
 A:Title: Purification and chemical characterization of peptide G-1, an invertebrate neur
 A:Reference number: A60216; MUID:90347460; PMID:2384751
 A:Accession: A60216
 A:Molecule type: protein
 A:Residues: 1-38 <PAV>
 C:Superfamily: hyperglycemic hormone
 C:Keywords: hormone

Query Match 22.1%; Score 21; DB 2; Length 38;
 Best Local Similarity 75.0%; Pred. No. 8e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 VCQD 11
 | | |
 Db 9 VCED 12

RESULT 14
 T08107
 nonenzymatic protein CP12 - Chlamydomonas reinhardtii (fragment)
 C:Species: Chlamydomonas reinhardtii
 C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
 C:Accession: T08107
 R:Wedel, N.; Soll, J.
 Proc. Natl. Acad. Sci. U.S.A. 95, 9699-9704, 1998
 A:Title: Evolutionary conserved light regulation of Calvin cycle activity by NADPH-media
 A:Reference number: Z16360; MUID:98356221; PMID:9689144
 A:Accession: T08107
 A:Status: preliminary; translated from GB/EMBL/DBBJ
 A:Molecule type: mRNA
 A:Residues: 1-40 <WED>
 A:Cross-references: UNIPROT:O65775; EMBL:AJ005284; NID:g3123344; PIDN:CAA06467.1; PID:g3
 A:Experimental source: strain cw15
 C:Comment: It is supposed that light regulation of Calvin cycle activity via NADPH-media
 . The two key enzymes of the Calvin cycle, phosphoribulokinase (EC 2.7.1.19) and glycera
 nenzymatic peptide CP12.
 C:Genetics:
 A:Gene: cp12

Query Match 22.1%; Score 21; DB 2; Length 40;
 Best Local Similarity 60.0%; Pred. No. 8.3e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 DVCQD 11
 | | |
 Db 35 DYCKD 39

RESULT 15
 H71330
 hypothetical protein TP0382 - syphilis spirochete
 C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C:Accession: H71330
 R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A:Reference number: A71250; MUID:98332770; PMID:9665876
 A:Accession: H71330
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-40 <COL>
 A:Cross-references: UNIPROT:083397; GB:AE001217; GB:AE000520; NID:g3322656; PIDN:AAC6538
 A:Experimental source: strain Nichols
 C:Genetics:
 A:Gene: TP0382

Query Match 22.1%; Score 21; DB 2; Length 40;
 Best Local Similarity 75.0%; Pred. No. 8.3e+02;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 DVCQ 10
|||:
Db 15 DVCQ 18

RESULT 16
S23825
EG-I protein - human papillomavirus type 33 (fragment)
C:Species: human papillomavirus type 33
C:Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C:Accession: S23825; S23829
R:Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnenackers, H.F.J.; Raaphorst, P.M.C.; Me
submitted to the EMBL Data Library, January 1992
A:Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via b
A:Reference number: S19906
A:Accession: S23825
A:Molecule type: mRNA
A:Residues: 1-47 <SNI>
A:Cross-references: UNIPROT:Q81883; UNIPROT:Q81884; EMBL:X64084; NID:G60273; PIDN:CAA454
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger

Query Match 22.1%; Score 21; DB 2; Length 47;
Best Local Similarity 75.0%; Pred. No. 9.6e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 DVCQ 10
|||:
Db 2 DLCC 5

RESULT 17
I48943
cellular disintegrin-related protein 16-2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 16-Aug-2004
C:Accession: I48943
R:Weskamp, G.; Blobel, C.P.
Proc. Natl. Acad. Sci. U.S.A. 91, 2748-2751, 1994
A:Title: A new family of cellular proteins related to snake venom disintegrins.
A:Reference number: A53476; MUID:94195820; PMID:8146185
A:Accession: I48943
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-47 <RES>
A:Cross-references: UNIPROT:Q61072; EMBL:U06145; NID:G487138; PIDN:AAA18424.1; PID:G4871
C:Superfamily: disintegrin homology

Query Match 22.1%; Score 21; DB 2; Length 47;
Best Local Similarity 60.0%; Pred. No. 9.6e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 DVCQ 11
|||:
Db 28 DCCD 32

RESULT 18
I57670
folitropin receptor - mouse
N:Alternate names: follicle-stimulating hormone receptor
C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 13-Aug-1999
C:Accession: I57670
R:Huntanien, I.T.; Eskola, V.; Pakarinen, P.; Matikainen, T.; Sprengel, R.
Mol. Cell. Endocrinol. 88, 55-66, 1992
A:Title: The murine luteinizing hormone and follicle-stimulating hormone receptor genes:
A:Reference number: I57670; MUID:93093308; PMID:1459341
A:Accession: I57670
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA

A:Residues: 1-51 <RES>
A:Cross-references: GB:S49632; NID:G261233; PIDN:AA824401.1; PID:G261234
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat i

Query Match 22.1%; Score 21; DB 2; Length 51;
Best Local Similarity 75.0%; Pred. No. 1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 VCQD 11
|||:
Db 31 LCQD 34

RESULT 19
B25507
proteinase inhibitor (Bowman-Birk) II-4 - wheat (fragment)
C:Species: Triticum aestivum (common wheat)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: B25507
R:Odani, S.; Koide, T.; Ono, T.
J. Biochem. 100, 975-983, 1986
A:Title: Wheat germ trypsin inhibitors. Isolation and structural characterization of si
A:Reference number: A91908; MUID:87137364; PMID:3818572
A:Accession: B25507
A:Molecule type: protein
A:Residues: 1-53 <ODA>
A:Cross-references: UNIPROT:P09864
C:Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
F:8-33/Domain: Bowman-Birk inhibitor repeat homology <BB3>

Query Match 22.1%; Score 21; DB 2; Length 53;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 VCQD 11
|||:
Db 48 VCED 51

RESULT 20
T07225
hypothetical protein 53 - Chlorella vulgaris chloroplast
C:Species: chloroplast Chlorella vulgaris
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C:Accession: T07225
R:Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Naka
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A:Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chl
A:Reference number: Z15985; MUID:97303241; PMID:9159184
A:Accession: T07225
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-53 <WAK>
A:Cross-references: EMBL:AB001684; NID:G2224352; PIDN:BAAS7872.1; PID:G2224388
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match 22.1%; Score 21; DB 2; Length 53;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 VCQD 11
|||:
Db 46 LCQD 49

RESULT 21
T41761
hypothetical protein 7a - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C:Species: Bombyx mori nuclear polyhedrosis virus, BMSNPV
A:Variety: isolate T3
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T41761
 R;Gomi, S.; Majima, K.; Maeda, S.
 J. Gen. Virol. 80, 1323-1337, 1999
 A;Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
 A;Reference number: Z22020; MUID:9281911; PMID:10355780
 A;Accession: T41761
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-53 <KAM>
 A;Cross-references: UNIPROT:Q92383; EMBL:L33180; PIDN:AAC63690.1
 A;Experimental source: isolate f3
 C;Genetics:
 A;Note: Orf_7a

Query Match 22.1%; Score 21; DB 2; Length 53;
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VCQD 11
 :|||
 Db 32 LCQD 35

RESULT 22
 T03654
 N;Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - maize (fragment)
 A;Alternate names: hypothetical protein Q
 C;Species: Zea mays (maize)
 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
 A;Accession: T03654
 R;Keith, C.S.; Hoang, D.O.; Barrett, B.M.; Feigelman, B.; Nelson, M.C.; Thai, H.; Baysdc
 Plant Physiol. 101, 329-332, 1993
 A;Title: Partial sequence analysis of 130 randomly selected maize cDNA clones.
 A;Reference number: Z14989; MUID:94105294; PMID:8278499
 A;Accession: T03654
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-57 <KEI>
 A;Cross-references: UNIPROT:Q08060; EMBL:M95076; NID:g168567; PIDN:AAA72117.1; PID:g1685
 C;Function:
 A;Description: catalyzes the oxidative phosphorylation of D-glyceraldehyde-3-phosphate b
 A;Pathway: glycolysis
 C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
 C;Keywords: oxidoreductase

Query Match 22.1%; Score 21; DB 2; Length 57;
 Best Local Similarity 60.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 DVCQD 11
 :|||
 Db 41 DFCKD 45

RESULT 23
 Z5BP83
 gene 58 protein - phase Pf3
 C;Species: phase Pf3
 A;Note: host Pseudomonas aeruginosa
 C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
 C;Accession: A04237
 R;Luiteman, R.G.M.; Putterman, D.G.; Schoenmakers, J.G.G.; Konings, R.N.H.; Day, L.A.
 J. Virol. 56, 268-276, 1985
 A;Title: Nucleotide sequence of the genome of Pf3, an IncP-1 plasmid-specific filamentou
 A;Reference number: A94693; MUID:85293231; PMID:3928901
 A;Accession: A04237
 A;Molecule type: DNA
 A;Residues: 1-58 <LUI>
 A;Cross-references: UNIPROT:P03629; GB:M11912; NID:Q215371; PIDN:AAA88377.1; PID:g215372
 C;Comment: Bacteriophage Pf3 is a class II filamentous phage.
 C;Comment: The host is strain O harboring IncP1 plasmids.
 C;Genetics:
 A;Gene: 58

C;Superfamily: class II filamentous phage gene 58 protein

Query Match 22.1%; Score 21; DB 1; Length 58;
 Best Local Similarity 60.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 DVCQD 11
 :|||
 Db 12 DVCHE 16

RESULT 24
 C69303
 ferredoxin (fdx-4) homolog - Archaeoglobus fulgidus
 C;Species: Archaeoglobus fulgidus
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 12-Jul-2004
 A;Accession: C69303
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artisch, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A;Reference number: A69250; MUID:98049343; PMID:9389475
 A;Accession: C69303
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-63 <KLB>
 A;Cross-references: UNIPROT:O29822; GB:AE001075; GB:AE000782; NID:G2689398; PIDN:AAB9081
 F:4-60/Domain: ferredoxin 2[4Fe-4S] homology <FER>

Query Match 22.1%; Score 21; DB 2; Length 63;
 Best Local Similarity 75.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQ 10
 :|||
 Db 60 DVCE 63

RESULT 25
 S05677
 hirudin IIb - medicinal leech
 N;Alternate names: thrombin inhibitor
 C;Species: Hirudo medicinalis (medicinal leech)
 C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S05677
 R;Scharf, M.; Engels, J.; Tripiet, D.
 FEBS Lett. 255, 105-110, 1989
 A;Title: Primary structures of new 'iso-hirudins'.
 A;Reference number: S05671; MUID:90005945; PMID:2792365
 A;Accession: S05677
 A;Molecule type: protein
 A;Residues: 1-65 <SCH>
 A;Cross-references: UNIPROT:P28510
 C;Superfamily: thrombin inhibitor, hirudin type
 C;Keywords: anticoagulant; serine proteinase inhibitor; sulfoprotein
 F:6-14,16-28,22-39/Disulfide bonds: #status predicted
 F:63/Binding site: sulfate (Tyr) (covalent) #status predicted

Query Match 22.1%; Score 21; DB 2; Length 65;
 Best Local Similarity 75.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VCQD 11
 :|||
 Db 15 LCQD 18

Search completed: June 30, 2005, 11:54:52
 Job time : 41.7531 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2005, 11:49:03 ; Search time 180.617 Seconds
(without alignments)
149.519 Million cell updates/sec

Title: US-09-743-684A-45
Perfect score: 95
Sequence: 1 XXXXXVQDXXXXXXXXXXXXX.....XXXXXXXXXXXXXXXXXXXX 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1722976 seqs, 385795295 residues

Total number of hits satisfying chosen parameters: 616042

Minimum DB seq length: 0
Maximum DB seq length: 71

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %	Score	Match	Length	ID	Description
1	30	31.6	20	17	US-10-690-276-716	Sequence 716, App
2	30	31.6	50	17	US-10-690-276-721	Sequence 721, App
3	27	28.4	37	16	US-10-425-115-193786	Sequence 193786, App
4	27	28.4	40	14	US-10-153-344-207	Sequence 27, Appl
5	27	28.4	48	10	US-09-774-639-204	Sequence 204, App
6	27	28.4	48	10	US-09-969-730-206	Sequence 206, App
7	27	28.4	48	15	US-10-621-363-206	Sequence 206, App
8	27	28.4	48	15	US-09-864-761-37337	Sequence 37337, A
9	27	28.4	61	15	US-10-424-599-247518	Sequence 247518, App
10	27	28.4	66	15	US-10-424-599-204388	Sequence 204388, App
11	26	27.4	47	9	US-09-864-761-33503	Sequence 33503, A

48	16	US-10-425-115-186090	Sequence 186090, App
54	16	US-10-425-115-338066	Sequence 338066, App
56	16	US-10-437-963-194844	Sequence 194844, App
36	10	US-09-892-877-283	Sequence 283, App
36	10	US-09-948-783-295	Sequence 295, App
44	15	US-10-424-599-199151	Sequence 199151, App
44	16	US-10-425-115-203275	Sequence 203275, App
49	14	US-10-029-386-34119	Sequence 34119, A
50	15	US-10-424-599-206216	Sequence 206216, App
52	9	US-09-796-692-787	Sequence 787, App
52	9	US-09-796-692-1428	Sequence 1428, App
52	9	US-09-796-692-1892	Sequence 1892, App
52	14	US-10-040-862-787	Sequence 787, App
52	14	US-10-040-862-1428	Sequence 1428, App
52	14	US-10-040-862-1892	Sequence 1892, App
52	15	US-10-057-475B-787	Sequence 787, App
52	15	US-10-057-475B-1428	Sequence 1428, App
52	15	US-10-057-475B-1892	Sequence 1892, App
52	15	US-10-154-884B-787	Sequence 787, App
52	15	US-10-154-884B-1428	Sequence 1428, App
52	15	US-10-154-884B-1892	Sequence 1892, App
52	15	US-10-424-599-222152	Sequence 222152, App
52	16	US-10-764-324-787	Sequence 787, App
52	16	US-10-764-324-1428	Sequence 1428, App
52	16	US-10-764-324-1892	Sequence 1892, App
57	16	US-10-425-115-278638	Sequence 278638, App
59	15	US-10-424-599-173624	Sequence 173624, App
62	15	US-10-424-599-245290	Sequence 245290, App
64	15	US-10-424-599-257942	Sequence 257942, App
64	16	US-10-425-115-331929	Sequence 331929, App
65	16	US-10-425-115-336508	Sequence 336508, App
66	16	US-10-425-115-337941	Sequence 337941, App
9	8	US-08-344-824-318	Sequence 318, App
10	8	US-08-344-824-192	Sequence 192, App
14	15	US-10-390-585-33	Sequence 33, Appl
14	15	US-10-390-585-40	Sequence 40, Appl
17	15	US-10-385-394-243	Sequence 243, Appl
17	18	US-10-846-341-11	Sequence 11, Appl
18	17	US-10-659-207-203	Sequence 203, Appl
20	14	US-10-397-411-12	Sequence 12, Appl
20	16	US-10-776-013-576	Sequence 576, App
22	15	US-10-390-585-54	Sequence 54, Appl
22	15	US-10-639-067-95	Sequence 95, Appl
30	15	US-10-296-734-612	Sequence 612, App
30	15	US-10-296-734-614	Sequence 614, App
30	15	US-10-296-734-1074	Sequence 1074, App
30	15	US-10-296-734-1076	Sequence 1076, App
32	17	US-10-652-364-2	Sequence 2, Appli
35	14	US-10-252-734-24	Sequence 24, Appl
35	14	US-10-252-734-25	Sequence 25, Appl
39	9	US-09-864-761-48369	Sequence 48369, A
39	16	US-10-425-115-222371	Sequence 222371, App
41	15	US-10-424-599-193911	Sequence 193911, App
43	15	US-10-424-599-175677	Sequence 175677, App
43	15	US-10-425-115-279723	Sequence 279723, App
45	15	US-10-623-629-3	Sequence 3, Appli
46	10	US-09-764-891-5050	Sequence 5050, App
47	15	US-10-424-599-243874	Sequence 243874, App
48	17	US-10-652-364-4	Sequence 4, Appli
48	16	US-10-408-765A-63	Sequence 63, Appl
49	16	US-10-425-115-311828	Sequence 311828, App
50	9	US-09-864-761-39226	Sequence 39226, A
50	16	US-10-425-115-290845	Sequence 290845, App
51	16	US-10-425-115-348186	Sequence 348186, App
52	16	US-10-425-115-208058	Sequence 208058, App
53	15	US-10-424-599-233885	Sequence 233885, App
54	15	US-10-424-599-233631	Sequence 233631, App
55	16	US-10-437-963-166269	Sequence 166269, App
58	13	US-10-001-835-178	Sequence 178, App
58	15	US-10-424-599-182927	Sequence 182927, App
58	16	US-10-437-963-132662	Sequence 132662, App
58	15	US-10-425-115-338986	Sequence 338986, App
59	15	US-10-424-599-217360	Sequence 217360, App

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 86 24 25.3 61 10 US-09-498-272-61 Sequence 61, Appl
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 88 24 25.3 62 15 US-10-381-752-31 Sequence 31, Appl
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 90 24 25.3 63 16 US-10-425-115-225902 Sequence 225902,
 91 24 25.3 64 15 US-10-381-752-21 Sequence 21, Appl
 92 24 25.3 64 15 US-10-381-752-22 Sequence 22, Appl
 93 24 25.3 64 16 US-10-425-115-211378 Sequence 211378,
 94 24 25.3 65 16 US-10-425-115-310245 Sequence 310245,
 95 24 25.3 66 11 US-09-864-408A-4602 Sequence 4602, Ap
 96 24 25.3 66 15 US-10-424-599-151029 Sequence 151029,
 97 24 25.3 66 15 US-10-424-599-264913 Sequence 264913,
 98 24 25.3 67 17 US-10-886-384-17 Sequence 17, Appl
 99 24 25.3 67 16 US-10-437-963-172874 Sequence 172874,
 100 24 25.3 68 15 US-10-623-629-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
 US-10-690-276-716
 ; Sequence 716, Application US/10690276
 ; Publication No. US20050112118A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Incorporated
 ; APPLICANT: Cimbora, Daniel
 ; APPLICANT: Heichman, Karen
 ; APPLICANT: Bartel, Paul
 ; APPLICANT: Mauck, Kimberly
 ; APPLICANT: Bush, Angie
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFLAMMATORY DISORDERS
 ; FILE REFERENCE: 1834.01
 ; CURRENT APPLICATION NUMBER: US/10/690,276
 ; CURRENT FILING DATE: 2003-10-20
 ; PRIOR APPLICATION NUMBER: 09/727,384
 ; PRIOR FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: 60/168,377
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: 60/168,379
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: 60/185,056
 ; PRIOR FILING DATE: 2000-02-25
 ; PRIOR APPLICATION NUMBER: 10/035,344
 ; PRIOR FILING DATE: 2002-01-04
 ; PRIOR APPLICATION NUMBER: 60/259,571
 ; PRIOR FILING DATE: 2001-01-04
 ; PRIOR APPLICATION NUMBER: 10/035,343
 ; PRIOR FILING DATE: 2002-01-04
 ; PRIOR APPLICATION NUMBER: 60/259,572
 ; PRIOR FILING DATE: 2001-01-04
 ; PRIOR APPLICATION NUMBER: 10/099,924
 ; PRIOR FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: 60/276,179
 ; PRIOR FILING DATE: 2001-03-15
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 728
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 716
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-690-276-716

Query Match 31.6%; Score 30; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 DVCQD 11
 Db 16 DVCQD 20

RESULT 2
 US-10-690-276-721
 ; Sequence 721, Application US/10690276
 ; Publication No. US20050112118A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Incorporated
 ; APPLICANT: Cimbora, Daniel
 ; APPLICANT: Heichman, Karen
 ; APPLICANT: Bartel, Paul
 ; APPLICANT: Mauck, Kimberly
 ; APPLICANT: Bush, Angie
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFLAMMATORY DISORDERS
 ; FILE REFERENCE: 1834.01
 ; CURRENT APPLICATION NUMBER: US/10/690,276
 ; CURRENT FILING DATE: 2003-10-20
 ; PRIOR APPLICATION NUMBER: 09/727,384
 ; PRIOR FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: 60/168,377
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: 60/168,379
 ; PRIOR FILING DATE: 1999-12-02
 ; PRIOR APPLICATION NUMBER: 60/185,056
 ; PRIOR FILING DATE: 2000-02-25
 ; PRIOR APPLICATION NUMBER: 10/035,344
 ; PRIOR FILING DATE: 2002-01-04
 ; PRIOR APPLICATION NUMBER: 60/259,571
 ; PRIOR FILING DATE: 2001-01-04
 ; PRIOR APPLICATION NUMBER: 10/035,343
 ; PRIOR FILING DATE: 2002-01-04
 ; PRIOR APPLICATION NUMBER: 60/259,572
 ; PRIOR FILING DATE: 2001-01-04
 ; PRIOR APPLICATION NUMBER: 10/099,924
 ; PRIOR FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: 60/276,179
 ; PRIOR FILING DATE: 2001-03-15
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 728
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 721
 ; LENGTH: 50
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-690-276-721
 Query Match 31.6%; Score 30; DB 17; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 DVCQD 11
 Db 46 DVCQD 50
 RESULT 3
 US-10-425-115-193786
 ; Sequence 193786, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 193786
 ; LENGTH: 37
 ; TYPE: PRT
 ; ORGANISM: Zea mays

FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_108314C.1.pcp
US-10-425-115-193786

Query Match 28.4%; Score 27; DB 16; Length 37;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 7 DVCQD 11
|:|
Db 11 DVCQD 15

RESULT 4
US-10-153-344-27
; Sequence 27, Application US/10153344
; Publication No. US20030004124A1
; GENERAL INFORMATION:
; APPLICANT: ROTHMAN, JOEL
; APPLICANT: BLOSS, TIM
; APPLICANT: WITZE, ERIC
; TITLE OF INVENTION: BTP3: AN INHIBITOR OF APOPTOSIS
; FILE REFERENCE: 407T-300410US
; CURRENT APPLICATION NUMBER: US/10/153,344
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/292,559
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (34)-(34)
; OTHER INFORMATION: X is any amino acid.
US-10-153-344-27

Query Match 28.4%; Score 27; DB 14; Length 40;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 7 DVCQD 11
|:|
Db 12 DVCQD 16

RESULT 5
US-09-774-639-204
; Sequence 204, Application US/09774639
; Publication No. US20030003555A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 204
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-639-204

Query Match 28.4%; Score 27; DB 10; Length 48;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 7 DVCQD 11

Db |:
28 DVCQD 32

RESULT 6
US-09-969-730-206
; Sequence 206, Application US/09969730
; Publication No. US2003005443A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P2
; CURRENT APPLICATION NUMBER: US/09/969,730
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,367
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,365
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/055,970
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,986
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,311
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,808
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,803
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,809
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,806
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,310
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,798
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,309
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,312
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,807
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,386
; PRIOR FILING DATE: 1997-08-05
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 206

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; LENGTH: 48
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-969-730-206

Query Match      28.4%; Score 27; DB 10; Length 48;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      7 DVCQD 11
Db      28 DLCQD 32

RESULT 7
US-10-621-363-206
; Sequence 206, Application US/10621363
; Publication No. US20040023283A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ0132C1
; CURRENT APPLICATION NUMBER: US/10/621,363
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 206
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-621-363-206

Query Match      28.4%; Score 27; DB 15; Length 48;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      7 DVCQD 11
Db      28 DLCQD 32

RESULT 8
US-09-864-761-37337
; Sequence 37337, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

```

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; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37337
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009721.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 9.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 9.6
; OTHER INFORMATION: EST_HUMAN HIT: B541441.1, EVALUATE 3.00e-25
; OTHER INFORMATION: SWISSPROT HIT: P25167, EVALUATE 2.00e-18
US-09-864-761-37337

Query Match      28.4%; Score 27; DB 9; Length 55;
Best Local Similarity 80.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      7 DVCQD 11
Db      32 DVCED 36

RESULT 9
US-10-424-599-247518
; Sequence 247518, Application US/10424599

```

Publication No. US20040031072A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa Thomas J
 APPLICANT: Kovalic David K
 APPLICANT: Zhou Yihua
 APPLICANT: Cao Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53223)B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO 247518
 LENGTH: 61
 TYPE: PRT
 ORGANISM: Glycine max
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)-(61)
 OTHER INFORMATION: unsure at all Xaa locations
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_65538C.1.pap
 US-10-424-599-247518

Query Match 28.4%; Score 27; DB 15; Length 61;
 Best Local Similarity 80.0%; Pred. No. 6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
 :|||
 Db 40 DMCQD 44

RESULT 10
 US-10-424-599-204388
 Sequence 204388, Application US/10424599
 Publication No. US20040031072A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa Thomas J
 APPLICANT: Kovalic David K
 APPLICANT: Zhou Yihua
 APPLICANT: Cao Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53223)B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO 204388
 LENGTH: 66
 TYPE: PRT
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_2658C.1.pap
 US-10-424-599-204388

Query Match 28.4%; Score 27; DB 15; Length 66;
 Best Local Similarity 80.0%; Pred. No. 6.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
 :|||
 Db 42 DLQCD 46

RESULT 11
 US-09-864-761-33503
 Sequence 33503, Application US/09864761
 Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 FILE REFERENCE: Aecmica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 33503
 LENGTH: 47
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AL035681.13
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
 OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 3.8
 OTHER INFORMATION: EST_HUMAN HIT: AL120419.1, EVALUE 3.00e-23
 OTHER INFORMATION: EST_HUMAN HIT: AL120211.1, EVALUE 2.00e-23
 OTHER INFORMATION: SWISSPROT HIT: P54725, EVALUE 2.70e+00
 US-09-864-761-33503

Query Match 27.4%; Score 26; DB 9; Length 47;
 Best Local Similarity 80.0%; Pred. No. 7.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 DVCQD 11
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 Db 22 DTCQD 26

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RESULT 12
US-10-425-115-186090
; Sequence 186090, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 186090
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_101304C.1.pep
US-10-425-115-186090

Query Match      27.4%; Score 26; DB 16; Length 48;
Best Local Similarity 80.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      7 DVCQD 11
Db      42 DVCRD 46

RESULT 13
US-10-425-115-338066
; Sequence 338066, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 338066
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_71482C.1.pep
US-10-425-115-338066

Query Match      27.4%; Score 26; DB 16; Length 54;
Best Local Similarity 80.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      7 DVCQD 11
Db      30 DVCCKD 34

RESULT 14
US-10-437-963-194844
; Sequence 194844, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
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; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 194844
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_90850C.1.pep
US-10-437-963-194844

Query Match      27.4%; Score 26; DB 16; Length 56;
Best Local Similarity 80.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      7 DVCQD 11
Db      11 DVCCKD 15

RESULT 15
US-09-892-877-283
; Sequence 283, Application US/09892877
; Publication No. US20030077809A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 97 Human secreted proteins
; FILE REFERENCE: P2028P1
; CURRENT APPLICATION NUMBER: US/09/892,877
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 283
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-877-283

Query Match      26.3%; Score 25; DB 10; Length 36;
Best Local Similarity 80.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 DVCQD 11
Db      16 DVCSD 20

RESULT 16
US-09-948-783-295
; Sequence 295, Application US/09948783
; Publication No. US20030100051A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 97 Human secreted proteins
; FILE REFERENCE: P2028P2
; CURRENT APPLICATION NUMBER: US/09/948,783
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,846
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: 09/892,877
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/437,658
; PRIOR FILING DATE: 1999-11-10
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PRIOR APPLICATION NUMBER: PCT/US99/09847
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085,093
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085,094
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085,105
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085,180
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085,927
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,906
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,924
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,922
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,921
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,923
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,925
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,928
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,920
PRIOR FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 465
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 295
LENGTH: 36
TYPE: PRT
ORGANISM: Homo sapiens
US-09-948-783-295

Query Match 26.3%; Score 25; DB 10; Length 36;
Best Local Similarity 80.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 DVCQD 11
Db 16 DVCSD 20

RESULT 17
US-10-424-599-199151
Sequence 199151, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 199151
LENGTH: 42
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(42)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_21858C.1.pep
US-10-424-599-199151

Query Match 26.3%; Score 25; DB 15; Length 42;

Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 7 DVCQD 11
Db 4 DICQE 8
RESULT 18
US-10-425-115-203275
Sequence 203275, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 203275
LENGTH: 44
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_116974C.1.pep
US-10-425-115-203275

Query Match 26.3%; Score 25; DB 16; Length 44;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 DVCQD 11
Db 16 DVCSD 20

RESULT 19
US-10-029-386-34119
Sequence 34119, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: AEOmica-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 34119
LENGTH: 49
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006427.13
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.38
US-10-029-386-34119

Query Match 26.3%; Score 25; DB 14; Length 49;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 DVCQD 11
Db 37 DFCQD 41

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RESULT 20
US-10-424-599-206216
; Sequence 206216, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 206216
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_2823C.1.pgp
US-10-424-599-206216

Query Match      26.3%; Score 25; DB 15; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 DVCQD 11
      |||||
Db      31 DVCQD 35

RESULT 21
US-09-796-692-787
; Sequence 787, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-03-17
; PRIOR FILING DATE: 2000-03-17
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-04-28
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; PRIOR FILING DATE: 2000-05-01
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; PRIOR FILING DATE: 2000-05-22
; PRIOR FILING DATE: 2000-05-22
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-08-04
; PRIOR FILING DATE: 2000-08-04
; PRIOR FILING DATE: 2000-08-07
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 787
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(52)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-796-692-787

Query Match      26.3%; Score 25; DB 9; Length 52;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 DVCQD 11
      |||||
Db      36 DVCQD 40
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(52)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-796-692-787

Query Match      26.3%; Score 25; DB 9; Length 52;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 DVCQD 11
      |||||
Db      36 DVCQD 40

RESULT 22
US-09-796-692-1428
; Sequence 1428, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-03-17
; PRIOR FILING DATE: 2000-03-17
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-22
; PRIOR FILING DATE: 2000-05-22
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-08-04
; PRIOR FILING DATE: 2000-08-04
; PRIOR FILING DATE: 2000-08-07
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1428
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(52)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-796-692-1428

Query Match      26.3%; Score 25; DB 9; Length 52;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 DVCQD 11
      |||||
Db      36 DVCQD 40
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```
RESULT 23
US-09-796-692-1892
; Sequence 1892, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR FILING DATE: 2001-03-01
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-03-17
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; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-08-04
; PRIOR FILING DATE: 2000-08-04
; PRIOR FILING DATE: 2000-08-07
; PRIOR FILING DATE: 2000-08-07
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1892
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: variant
; LOCATION: (1)...(52)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-796-692-1892

Query Match          26.3%; Score 25; DB 9; Length 52;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 36 DVCQD 40

RESULT 24
US-10-040-862-787
; Sequence 787, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-0135200S
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-03-17
; PRIOR FILING DATE: 2000-03-17
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-22
; PRIOR FILING DATE: 2000-05-22
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-08-04
; PRIOR FILING DATE: 2000-08-04
; PRIOR FILING DATE: 2000-08-07
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1892
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: variant
; LOCATION: (1)...(52)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-796-692-1892

Query Match          26.3%; Score 25; DB 9; Length 52;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 36 DVCQD 40

RESULT 25
US-10-040-862-1428
; Sequence 1428, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-0135200S
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-03-17
; PRIOR FILING DATE: 2000-03-17
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-05-01
; PRIOR FILING DATE: 2000-05-01
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; PRIOR FILING DATE: 2000-05-22
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-08-04
; PRIOR FILING DATE: 2000-08-04
; PRIOR FILING DATE: 2000-08-07
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 787
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: variant
; LOCATION: (1)...(52)
; OTHER INFORMATION: Xaa = Any amino acid
US-10-040-862-787

Query Match          26.3%; Score 25; DB 14; Length 52;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 36 DVCQD 40

RESULT 26
US-10-040-862-1428
; Sequence 1428, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-0135200S
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-03-17
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; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-08-04
; PRIOR FILING DATE: 2000-08-04
; PRIOR FILING DATE: 2000-08-07
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 787
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: variant
; LOCATION: (1)...(52)
; OTHER INFORMATION: Xaa = Any amino acid
US-10-040-862-787
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; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1428
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(52)
; OTHER INFORMATION: Xaa = Any amino acid
US-10-040-862-1428
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Query Match          26.3%; Score 25; DB 14; Length 52;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Qy      7 DVCQD 11
        |||
Db      36 DVCND 40
```

Search completed: June 30, 2005, 12:02:15
Job time : 182.617 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2005, 11:37:42 ; Search time 51.8518 Seconds
(without alignments)
100.77% Million cell updates/sec

Title: US-09-743-684A-45
Perfect score: 95
Sequence: 1 XXXXXVCQXXXXXXXXXXXXXXXXXXXXXXXXXXXX 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 298299

Minimum DB seq length: 0
Maximum DB seq length: 71

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	31.6	5	4	US-09-352-548-28
2	30	31.6	6	4	US-09-352-548-27
3	30	31.6	7	4	US-09-352-548-26
4	30	31.6	8	4	US-09-352-548-25
5	30	31.6	9	4	US-09-352-548-24
6	30	31.6	10	4	US-09-352-548-21
7	30	31.6	11	4	US-09-352-548-19
8	30	31.6	11	4	US-09-352-548-33
9	30	31.6	15	2	US-08-584-671-4
10	30	31.6	15	3	US-09-027-376-4
11	30	31.6	15	3	US-09-094-192-4
12	30	31.6	15	4	US-09-352-548-13
13	30	31.6	16	4	US-09-352-548-47
14	30	31.6	16	4	US-09-352-548-48
15	30	31.6	16	4	US-09-352-548-54
16	30	31.6	16	4	US-09-352-548-55
17	30	31.6	16	4	US-09-352-548-56
18	30	31.6	16	4	US-09-352-548-57
19	30	31.6	16	4	US-09-352-548-58
20	30	31.6	16	4	US-09-352-548-59
21	30	31.6	19	2	US-08-584-671-5
22	30	31.6	19	3	US-09-027-376-5
23	30	31.6	19	3	US-09-094-192-5
24	30	31.6	70	4	US-09-352-548-44
25	30	31.6	70	4	US-09-352-548-45
26	30	31.6	70	4	US-09-352-548-46
27	30	31.6	70	4	US-09-352-548-49

28	30	31.6	70	4	US-09-352-548-50	Sequence 50, Appl
29	30	31.6	70	4	US-09-352-548-51	Sequence 51, Appl
30	30	31.6	70	4	US-09-352-548-52	Sequence 52, Appl
31	30	31.6	70	4	US-09-352-548-53	Sequence 53, Appl
32	29	30.5	5	4	US-09-352-548-36	Sequence 36, Appl
33	27	28.4	5	4	US-09-352-548-37	Sequence 37, Appl
34	27	28.4	5	4	US-09-352-548-39	Sequence 39, Appl
35	27	28.4	48	4	US-09-774-639-204	Sequence 204, Appl
36	26	27.4	5	4	US-09-352-548-35	Sequence 35, Appl
37	26	27.4	64	4	US-09-248-796A-25050	Sequence 25050, A
38	26	27.4	69	4	US-09-248-796A-28064	Sequence 28064, A
39	25	26.3	5	4	US-09-352-548-38	Sequence 38, Appl
40	25	26.3	5	4	US-09-352-548-40	Sequence 40, Appl
41	24	25.3	5	4	US-09-352-548-22	Sequence 22, Appl
42	24	25.3	9	4	US-09-352-548-29	Sequence 29, Appl
43	24	25.3	15	2	US-08-476-062A-29	Sequence 29, Appl
44	24	25.3	15	5	PCT-US96-01314-29	Sequence 29, Appl
45	24	25.3	17	3	US-08-163-919A-11	Sequence 11, Appl
46	24	25.3	17	4	US-08-462-515-11	Sequence 11, Appl
47	24	25.3	17	5	PCT-US94-14073-11	Sequence 11, Appl
48	24	25.3	18	3	US-08-477-928A-26	Sequence 26, Appl
49	24	25.3	18	4	US-09-620-091-203	Sequence 203, Appl
50	24	25.3	26	2	US-08-620-151-84	Sequence 84, Appl
51	24	25.3	40	2	US-08-751-305-5	Sequence 5, Appl
52	24	25.3	41	6	5177197-45	Patent No. 5177197
53	24	25.3	41	6	5177197-45	Patent No. 5177197
54	24	25.3	44	1	US-08-421-661-4	Sequence 4, Appl
55	24	25.3	50	4	US-09-270-767-46220	Sequence 46220, A
56	24	25.3	51	1	US-07-707-542E-6	Sequence 6, Appl
57	24	25.3	60	4	US-09-248-796A-19465	Sequence 19465, A
58	24	25.3	61	2	US-08-465-380-61	Sequence 61, Appl
59	24	25.3	61	2	US-08-486-397-61	Sequence 61, Appl
60	24	25.3	61	2	US-08-486-399-61	Sequence 61, Appl
61	24	25.3	61	2	US-08-461-965-61	Sequence 61, Appl
62	24	25.3	61	2	US-08-634-641-61	Sequence 61, Appl
63	24	25.3	61	3	US-09-249-471-61	Sequence 61, Appl
64	24	25.3	61	3	US-09-249-472-61	Sequence 61, Appl
65	24	25.3	61	3	US-09-249-451-61	Sequence 61, Appl
66	24	25.3	61	3	US-08-809-455-61	Sequence 61, Appl
67	24	25.3	61	3	US-09-249-461-61	Sequence 61, Appl
68	24	25.3	61	3	US-09-249-448-61	Sequence 61, Appl
69	24	25.3	61	4	US-09-249-473-61	Sequence 61, Appl
70	24	25.3	65	4	US-09-248-796A-23463	Sequence 23463, A
71	24	25.3	66	4	US-09-497-822C-17	Sequence 17, Appl
72	24	25.3	71	2	US-08-377-432-8	Sequence 8, Appl
73	24	25.3	71	4	US-08-900-241-8	Sequence 8, Appl
74	23	24.2	9	3	US-09-510-738A-38	Sequence 38, Appl
75	23	24.2	9	4	US-09-861-966-38	Sequence 38, Appl
76	23	24.2	9	4	US-09-341-982-19	Sequence 19, Appl
77	23	24.2	9	4	US-09-341-982-70	Sequence 70, Appl
78	23	24.2	9	4	US-09-341-982-73	Sequence 73, Appl
79	23	24.2	10	1	US-09-919-048-38	Sequence 38, Appl
80	23	24.2	10	1	US-08-483-880-27	Sequence 27, Appl
81	23	24.2	10	2	US-08-273-274-27	Sequence 27, Appl
82	23	24.2	10	2	US-08-475-041-27	Sequence 27, Appl
83	23	24.2	10	2	US-08-335-832-45	Sequence 45, Appl
84	23	24.2	10	2	US-08-484-773-27	Sequence 27, Appl
85	23	24.2	10	4	US-09-341-982-37	Sequence 37, Appl
86	23	24.2	12	4	US-09-341-982-10	Sequence 10, Appl
87	23	24.2	12	4	US-09-341-982-76	Sequence 76, Appl
88	23	24.2	12	4	US-09-341-982-79	Sequence 79, Appl
89	23	24.2	13	2	US-08-335-832-26	Sequence 26, Appl
90	23	24.2	13	2	US-08-335-832-27	Sequence 27, Appl
91	23	24.2	17	1	US-08-077-256-2	Sequence 2, Appl
92	23	24.2	17	1	US-08-259-672-2	Sequence 2, Appl
93	23	24.2	17	1	US-08-459-351-2	Sequence 2, Appl
94	23	24.2	17	1	US-08-460-533-2	Sequence 2, Appl
95	23	24.2	17	5	PCT-US94-06654-2	Sequence 2, Appl
96	23	24.2	20	1	US-08-488-212A-28	Sequence 28, Appl
97	23	24.2	20	1	US-08-320-306-28	Sequence 28, Appl
98	23	24.2	20	2	US-08-488-209B-28	Sequence 28, Appl
99	23	24.2	20	2	US-08-408-011-28	Sequence 28, Appl
100	23	24.2	28	3	US-08-814-836-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-352-548-28
; Sequence 28, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-D6
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-28

Query Match 31.6%; Score 30; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
|
|
|
|
Db 1 DVCQD 5

RESULT 2
US-09-352-548-27
; Sequence 27, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-C7
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-27

Query Match 31.6%; Score 30; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
|
|
|
|
Db 1 DVCQD 5

RESULT 3
US-09-352-548-26

; Sequence 26, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-I8
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-26

Query Match 31.6%; Score 30; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
|
|
|
|
Db 1 DVCQD 5

RESULT 4
US-09-352-548-25
; Sequence 25, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-Q9
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-25

Query Match 31.6%; Score 30; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
|
|
|
|
Db 1 DVCQD 5

RESULT 5
US-09-352-548-24
; Sequence 24, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US

; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-M10
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-24

Query Match 31.6%; Score 30; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 1 DVCQD 5

RESULT 6

US-09-352-548-21
; Sequence 21, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431e1 Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-V11
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-21

Query Match 31.6%; Score 30; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 1 DVCQD 5

RESULT 7

US-09-352-548-19
; Sequence 19, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431e1 Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:G1-V11
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-19

Query Match 31.6%; Score 30; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 2 DVCQD 6

RESULT 8

US-09-352-548-33
; Sequence 33, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431e1 Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:G1-(S7)-V11
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-33

Query Match 31.6%; Score 30; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 2 DVCQD 6

RESULT 9

US-08-584-671-4
; Sequence 4, Application US/08584671
; Patent No. 5910568
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS

;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/584,671
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MONAHAN, THOMAS J
;; REGISTRATION NUMBER: 29835
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 814-865-6277
;; TELEFAX: 814-865-3591
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15
;; TYPE: AMINO ACID
;; STRANDEDNESS: SINGLE
;; TOPOLOGY: UNKNOWN
US-08-584-671-4

Query Match 31.6%; Score 30; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
|||
Db 9 DVCQD 13

RESULT 10

US-09-027-376-4
; Sequence 4, Application US/09027376
; Patent No. 6004586

; GENERAL INFORMATION:

; APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,

; APPLICANT: CRAMER, PALMER

; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM

; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE

; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA

; ADDRESSEE: STATE UNIVERSITY

; STREET: 113 TECHNOLOGY CENTER

; CITY: UNIVERSITY PARK

; STATE: PENNSYLVANIA

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 16802-7000

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: NEC 286

; OPERATING SYSTEM: DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/027,376

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/584,671

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: MONAHAN, THOMAS J

; REGISTRATION NUMBER: 29835

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 814-865-6277

; TELEFAX: 814-865-3591

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15

; TYPE: AMINO ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: UNKNOWN

US-09-027-376-4

Query Match 31.6%; Score 30; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
|||
Db 9 DVCQD 13

RESULT 11

US-09-094-192-4

; Sequence 4, Application US/09094192

; Patent No. 6103483

; GENERAL INFORMATION:

; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.

; APPLICANT: CRAMER, PALMER

; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM TO EGG SURFACES AND PROC:

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA STATE UNIVERSITY

; STREET: 113 TECHNOLOGY CENTER

; CITY: UNIVERSITY PARK

; STATE: PENNSYLVANIA

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 16802-7000

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: NEC 286

; OPERATING SYSTEM: DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/094,192

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MONAHAN, THOMAS J

; REGISTRATION NUMBER: 29835

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 814-865-6277

; TELEFAX: 814-865-3591

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15

; TYPE: AMINO ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: UNKNOWN

US-09-094-192-4

Query Match 31.6%; Score 30; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
|||
Db 9 DVCQD 13

RESULT 12

US-09-352-548-13

; Sequence 13, Application US/09352548

; Patent No. 6500431

; GENERAL INFORMATION:

; APPLICANT: Gill, Parkash S.

; APPLICANT: Parkash S. Gill, M.D., Inc.

; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth

; FILE REFERENCE: 017986-000410US

; CURRENT APPLICATION NUMBER: US/09/352,548

; CURRENT FILING DATE: 1999-07-12

; EARLIER APPLICATION NUMBER: US 60/092,647

; EARLIER FILING DATE: 1998-07-13

; NUMBER OF SEQ ID NOS: 59
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
 ; OTHER INFORMATION: polypeptide
 US-09-352-548-13

Query Match 31.6%; Score 30; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
 |||||
 Db 7 DVCQD 11

RESULT 13
 US-09-352-548-47
 ; Sequence 47, Application US/09352548
 ; Patent No. 6500431
 ; GENERAL INFORMATION:
 ; APPLICANT: Gill, Parkash S.
 ; APPLICANT: Parkash S. Gill, M.D., Inc.
 ; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
 ; FILE REFERENCE: 017986-000410US
 ; CURRENT APPLICATION NUMBER: US/09/352,548
 ; CURRENT FILING DATE: 1999-07-12
 ; EARLIER APPLICATION NUMBER: US 60/092,647
 ; EARLIER FILING DATE: 1998-07-13
 ; NUMBER OF SEQ ID NOS: 59
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 47
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
 ; OTHER INFORMATION: polypeptide
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)..(6)
 ; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-6 may be
 ; OTHER INFORMATION: present or absent
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (12)..(16)
 ; OTHER INFORMATION: Xaa = any amino acid
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (13)..(16)
 ; OTHER INFORMATION: Xaa at positions 13-16 may be present or absent
 US-09-352-548-47

Query Match 31.6%; Score 30; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
 |||||
 Db 7 DVCQD 11

RESULT 14
 US-09-352-548-48
 ; Sequence 48, Application US/09352548
 ; Patent No. 6500431
 ; GENERAL INFORMATION:
 ; APPLICANT: Gill, Parkash S.
 ; APPLICANT: Parkash S. Gill, M.D., Inc.

; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
 ; FILE REFERENCE: 017986-000410US
 ; CURRENT APPLICATION NUMBER: US/09/352,548
 ; CURRENT FILING DATE: 1999-07-12
 ; EARLIER APPLICATION NUMBER: US 60/092,647
 ; EARLIER FILING DATE: 1998-07-13
 ; NUMBER OF SEQ ID NOS: 59
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 48
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
 ; OTHER INFORMATION: polypeptide
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)..(6)
 ; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-6 may be
 ; OTHER INFORMATION: present or absent
 US-09-352-548-48

Query Match 31.6%; Score 30; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
 |||||
 Db 7 DVCQD 11

RESULT 15
 US-09-352-548-54
 ; Sequence 54, Application US/09352548
 ; Patent No. 6500431
 ; GENERAL INFORMATION:
 ; APPLICANT: Gill, Parkash S.
 ; APPLICANT: Parkash S. Gill, M.D., Inc.
 ; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
 ; FILE REFERENCE: 017986-000410US
 ; CURRENT APPLICATION NUMBER: US/09/352,548
 ; CURRENT FILING DATE: 1999-07-12
 ; EARLIER APPLICATION NUMBER: US 60/092,647
 ; EARLIER FILING DATE: 1998-07-13
 ; NUMBER OF SEQ ID NOS: 59
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 54
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
 ; OTHER INFORMATION: polypeptide
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)..(4)
 ; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
 ; OTHER INFORMATION: present or absent
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (5)-
 ; OTHER INFORMATION: Xaa = any amino acid
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (6)-
 ; OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (12)
 ; OTHER INFORMATION: Xaa = any amino acid
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (13)..(16)

; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 13-16 may
; OTHER INFORMATION: be present or absent
US-09-352-548-54

Query Match 31.6%; Score 30; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
|
|
|
|
Db 7 DVCQD 11

RESULT 16

US-09-352-548-55
; Sequence 55, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(4)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
; OTHER INFORMATION: present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (13)..(16)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 13-16 may
; OTHER INFORMATION: be present or absent
US-09-352-548-55

Query Match 31.6%; Score 30; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
|
|
|
|
Db 7 DVCQD 11

RESULT 17

US-09-352-548-56
; Sequence 56, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US

; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(4)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
; OTHER INFORMATION: present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (14)..(16)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 14-16 may
; OTHER INFORMATION: be present or absent
US-09-352-548-56

Query Match 31.6%; Score 30; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
|
|
|
|
Db 7 DVCQD 11

RESULT 18

US-09-352-548-57
; Sequence 57, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(4)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
; OTHER INFORMATION: present or absent
US-09-352-548-57

Qy 7 DVCQD 11
|
|
|
|
Db 7 DVCQD 11

FEATURE:
NAME/KEY: MOD_RES
LOCATION: (5)
OTHER INFORMATION: Xaa = any amino acid
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (6)
OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (12)..(13)
OTHER INFORMATION: Xaa = any amino acid
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (15)..(16)
OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 15 and 16
OTHER INFORMATION: may be present or absent

US-09-352-548-57

Query Match 31.6%; Score 30; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 7 DVCQD 11

RESULT 19
US-09-352-548-58
Sequence 58, Application US/09352548
Patent No. 6500431
GENERAL INFORMATION:
APPLICANT: Gill, Parkash S.
APPLICANT: Parkash S. Gill, M.D., Inc.
TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
FILE REFERENCE: 017986-000410US
CURRENT APPLICATION NUMBER: US/09/352,548
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: US 60/092,647
EARLIER FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
OTHER INFORMATION: polypeptide
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)-(4)
OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
OTHER INFORMATION: present or absent
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (5)
OTHER INFORMATION: Xaa = any amino acid
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (6)
OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (12)..(14)
OTHER INFORMATION: Xaa = any amino acid
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (16)
OTHER INFORMATION: Xaa = any amino acid, Xaa at position 16 may be
OTHER INFORMATION: present or absent

US-09-352-548-58

Query Match 31.6%; Score 30; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 7 DVCQD 11

RESULT 20

US-09-352-548-59
Sequence 59, Application US/09352548
Patent No. 6500431
GENERAL INFORMATION:
APPLICANT: Gill, Parkash S.
APPLICANT: Parkash S. Gill, M.D., Inc.
TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
FILE REFERENCE: 017986-000410US
CURRENT APPLICATION NUMBER: US/09/352,548
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: US 60/092,647
EARLIER FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 59
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
OTHER INFORMATION: polypeptide
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)-(4)
OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-4 may be
OTHER INFORMATION: present or absent
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (5)
OTHER INFORMATION: Xaa = any amino acid
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (6)
OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (12)..(15)
OTHER INFORMATION: Xaa = any amino acid
OTHER INFORMATION: Xaa = any amino acid

US-09-352-548-59

Query Match 31.6%; Score 30; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 7 DVCQD 11

RESULT 21

US-08-584-671-5
Sequence 5, Application US/08584671
Patent No. 5910568
GENERAL INFORMATION:
APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,
APPLICANT: CRAMER, PALMER
TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA

ADDRESSEE: STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,671
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONAHAN, THOMAS J
REGISTRATION NUMBER: 29835
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 814-865-6277
TELEFAX: 814-865-3591
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
US-08-584-671-5

Query Match 31.6%; Score 30; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 8 DVCQD 12

RESULT 22
US-09-027-376-5
; Sequence 5, Application US/09027376
; Patent No. 6004586
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,376
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/584,671
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835

REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 814-865-6277
TELEFAX: 814-865-3591
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
US-09-027-376-5

Query Match 31.6%; Score 30; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 8 DVCQD 12

RESULT 23
US-09-094-192-5
; Sequence 5, Application US/09094192
; Patent No. 6103483
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM TO EGG SURFACES AND PROC
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,192
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-09-094-192-5

Query Match 31.6%; Score 30; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 8 DVCQD 12

RESULT 24
US-09-352-548-44
; Sequence 44, Application US/09352548

; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; TITLE OF INVENTION: No. 6500431e1 Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(6)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-6 may be
; OTHER INFORMATION: present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)..(70)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 12-70 may
; OTHER INFORMATION: be present or absent
US-09-352-548-44

Query Match 31.6%; Score 30; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DVCQD 11
|||
Db 7 DVCQD 11

RESULT 25
US-09-352-548-45
; Sequence 45, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; TITLE OF INVENTION: No. 6500431e1 Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(5)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(4)
; OTHER INFORMATION: Xaa at positions 1-4 may be present or absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)

; OTHER INFORMATION: Xaa = Gly, Ala, Ser or Thr
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)..(70)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 12-70 may
; OTHER INFORMATION: be present or absent
US-09-352-548-45
Query Match 31.6%; Score 30; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 DVCQD 11
|||
Db 7 DVCQD 11

Search completed: June 30, 2005, 11:53:57
Job time : 51.8518 secs

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OM protein - protein search, using sw model

Run on: June 30, 2005, 11:36:37 ; Search time 198.765 Seconds
(without alignments)
136.207 Million cell updates/sec

Title: US-09-743-684A-45
Perfect score: 95
Sequence: 1 XXXXXVQDXXXXXXXXXXXXXXX.....XXXXXXXXXXXXXXXXXXXX 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1053335

Minimum DB seq length: 0
Maximum DB seq length: 71

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	31.6	5	AAV58700	Antiangio
2	30	31.6	6	AAV58699	Antiangio
3	30	31.6	7	AAV58698	Antiangio
4	30	31.6	8	AAV58697	Antiangio
5	30	31.6	9	AAV58696	Antiangio
6	30	31.6	10	AAV58693	Antiangio
7	30	31.6	11	AAV58705	Antiangio
8	30	31.6	11	AAV58691	Antiangio
9	30	31.6	15	AAV58687	Antiangio
10	30	31.6	15	AAV58685	Antiangio
11	30	31.6	19	AAV18588	Universal
12	29	30.5	5	AAV58708	Antiangio
13	27	28.4	5	AAV58709	Antiangio
14	27	28.4	5	AAV58711	Antiangio
15	27	28.4	40	ABP71131	B10 CARD
16	27	28.4	40	ADSO5060	Staphyloc
17	27	28.4	48	ADJ5478	Novel hum
18	27	28.4	48	ADJ5478	Novel hum
19	27	28.4	55	AAV17684	Peptide #
20	27	28.4	55	AAV36706	Peptide #
21	27	28.4	55	AAV30198	Peptide #
22	27	28.4	55	AAV30198	Peptide #
23	27	28.4	55	AAV30198	Peptide #
24	27	28.4	55	AAV69858	Human bon
25	27	28.4	55	AAV57463	Human bra

26	27	28.4	55	4	ABG51557	Human liv
27	27	28.4	55	4	AAV05345	Peptide #
28	27	28.4	55	5	ABG39490	Human pep
29	26	27.4	5	3	AAV58707	Antiangio
30	26	27.4	47	4	AAV13785	Peptide #
31	26	27.4	47	4	ABG32719	Peptide #
32	26	27.4	47	4	AAV26183	Peptide #
33	26	27.4	47	4	ABG27560	Human pep
34	26	27.4	47	4	ABG18205	Protein #
35	26	27.4	47	4	AAV65918	Human bon
36	26	27.4	47	4	AAV53537	Human bra
37	26	27.4	47	4	ABG47574	Human liv
38	26	27.4	47	4	AAV01530	Peptide #
39	26	27.4	47	5	ABG35554	Human pep
40	26	27.4	54	3	AAV83246	Delta 6 d
41	25	26.3	5	3	AAV58710	Antiangio
42	25	26.3	5	3	AAV58712	Antiangio
43	25	26.3	9	8	ADK08335	Human pap
44	25	26.3	10	8	ADK08375	Human pap
45	25	26.3	10	8	ADK08374	Human pap
46	25	26.3	14	1	AAV60041	Sequence
47	25	26.3	14	1	AAV91930	Junction
48	25	26.3	21	4	AAV66970	Mutant pr
49	25	26.3	21	4	AAV66979	Mutant pr
50	25	26.3	29	4	AAV66968	Mutant pr
51	25	26.3	29	4	AAV66967	Castor oi
52	25	26.3	36	3	AAV76281	Fragment
53	25	26.3	36	7	ADK11923	Human sec
54	25	26.3	49	8	ABO60485	Human gen
55	25	26.3	52	4	AAV80423	Human hae
56	25	26.3	52	4	AAV81064	Human hae
57	25	26.3	52	4	AAV81528	Human hae
58	25	26.3	56	4	AAU51158	Propionib
59	25	26.3	56	6	ABM47677	Propionib
60	25	26.3	63	4	ABG10437	Novel hum
61	24	25.3	5	3	AAV58694	Antiangio
62	24	25.3	6	5	ABG90472	Hominidae
63	24	25.3	8	4	AAV01662	Hepatit
64	24	25.3	8	4	AAV01129	Hepatit
65	24	25.3	8	4	AAV02689	Hepatit
66	24	25.3	9	2	AAV59214	Peptide f
67	24	25.3	9	3	AAV58701	Antiangio
68	24	25.3	9	4	AAV02398	Hepatit
69	24	25.3	9	4	AAV03136	Hepatit
70	24	25.3	9	4	AAV03442	Hepatit
71	24	25.3	9	4	AAV00994	Hepatit
72	24	25.3	9	4	AAV00319	Hepatit
73	24	25.3	9	4	AAV02804	Hepatit
74	24	25.3	9	4	AAV00136	Hepatit
75	24	25.3	9	4	AAV03688	Hepatit
76	24	25.3	9	4	AAV00891	Hepatit
77	24	25.3	9	8	ADK97676	Immunogen
78	24	25.3	10	2	AAV47967	Immunogen
79	24	25.3	10	4	AAV00995	Hepatit
80	24	25.3	10	4	AAV01130	Hepatit
81	24	25.3	10	4	AAV00137	Hepatit
82	24	25.3	10	4	AAV01899	Hepatit
83	24	25.3	11	4	AAV00892	Hepatit
84	24	25.3	11	4	AAV00098	Hepatit
85	24	25.3	11	4	AAV01957	Hepatit
86	24	25.3	11	4	AAV01131	Hepatit
87	24	25.3	11	4	AAV01159	Hepatit
88	24	25.3	11	4	AAV02383	Hepatit
89	24	25.3	11	4	AAV02014	Hepatit
90	24	25.3	11	4	AAV02795	Hepatit
91	24	25.3	11	4	AAV01988	Hepatit
92	24	25.3	14	7	ADK70203	Human pro
93	24	25.3	15	2	AAV02082	Beta-2 in
94	24	25.3	15	2	AAV02070	Human bet
95	24	25.3	15	4	AAV03497	Hepatit
96	24	25.3	15	4	AAV03190	Hepatit
97	24	25.3	15	4	AAV03707	Hepatit
98	24	25.3	15	4	AAV04058	Hepatit

99 24 25.3 16 7 ADF70210 Human pro
100 24 25.3 16 8 ADL26452 Synthetic

ALIGNMENTS

RESULT 1
ID AAY58700 standard; peptide; 5 AA.

AC AAY58700;
XX
DT 25-APR-2000 (first entry)
XX
DE Antiangiogenic peptide derived from saposin B.

XX Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
XX

OS Homo sapiens.
XX
FN WO200002902-A1.

XX
PD 20-JAN-2000.

XX 12-JUL-1999; 99WO-US015772.

XX 13-JUL-1998; 98US-0092647P.

XX (GILL/) GILL P S.

XX Gill PS;

XX WPI; 2000-171128/15.

XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
PT tumor growth.

XX Claim 4; Page 57; 78pp; English.

XX The present sequence is that of a claimed peptide, derived from human
CC saposin B, that has antiangiogenic activity. The invention is based on
CC the discovery that saposin B (see AAY58716), previously known to be
CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
CC and antitumour activity, and also has antiproliferative and antimigratory
CC activity against endothelial cells. This activity is conserved in cryptic
CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
CC synthetically prepared and used in vitro or in vivo for the treatment of
CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
CC (claimed). The polypeptides can also be used in conjunction with
CC cytotoxic moieties to selectively kill certain cell types, e.g. for
CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
CC malformation, nonunion fracture, arthritis and other connective tissue
CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
CC corneal graft neovascularization, pyogenic granuloma, retrolental
CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
CC vascular adhesions and hypertrophic scars

XX Sequence 5 AA;

Query Match 31.6%; Score 30; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 DVCQD 11
|||||
Db 1 DVCQD 5

RESULT 2

AAY58699
ID AAY58699 standard; peptide; 6 AA.

XX AAY58699;
XX
DT 25-APR-2000 (first entry)
XX
DE Antiangiogenic peptide derived from saposin B.

XX Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
XX

OS Homo sapiens.

XX WO200002902-A1.

XX 20-JAN-2000.

XX 12-JUL-1999; 99WO-US015772.

XX 13-JUL-1998; 98US-0092647P.

XX (GILL/) GILL P S.

XX Gill PS;

XX WPI; 2000-171128/15.

XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
PT tumor growth.

XX Disclosure; Page 19; 78pp; English.

XX The present sequence is that of a novel peptide, derived from human
CC saposin B, that has antiangiogenic activity. The invention is based on
CC the discovery that saposin B (see AAY58716), previously known to be
CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
CC and antitumour activity, and also has antiproliferative and antimigratory
CC activity against endothelial cells. This activity is conserved in cryptic
CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
CC synthetically prepared and used in vitro or in vivo for the treatment of
CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
CC (claimed). The polypeptides can also be used in conjunction with
CC cytotoxic moieties to selectively kill certain cell types, e.g. for
CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
CC malformation, nonunion fracture, arthritis and other connective tissue
CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
CC corneal graft neovascularization, pyogenic granuloma, retrolental
CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
CC vascular adhesions and hypertrophic scars

XX Sequence 6 AA;

Query Match 31.6%; Score 30; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 DVCQD 11
|||||
Db 1 DVCQD 5

RESULT 3

AAY58698
ID AAY58698 standard; peptide; 7 AA.

XX AAY58698;

XX 25-APR-2000 (first entry)

XX Antiangiogenic peptide derived from saposin B.

XX Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
XX

OS Homo sapiens.
 XX WO200002902-A1.
 PN XX
 XX 20-JAN-2000.
 PD XX
 XX 12-JUL-1999; 99WO-US015772.
 XX 13-JUL-1998; 98US-0092647P.
 PR XX
 XX (GILL/) GILL P S.
 PA XX
 XX Gill PS;
 PI XX
 XX WPI; 2000-171128/15.
 DR XX
 XX Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.
 PT XX
 XX Disclosure; Page 19; 78pp; English.
 PS XX
 XX The present sequence is that of a novel peptide, derived from human saposin B, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumor activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars
 XX Sequence 7 AA;
 SQ
 Query Match 31.6%; Score 30; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 DVCQD 11
 DB 1 DVCQD 5
 RESULT 4
 AAY58697
 ID AAY58697 standard; peptide; 8 AA.
 XX
 AC AAY58697;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Antiangiogenic peptide derived from saposin B.
 XX
 KW Antiangiogenic; angiogenesis inhibitor; antitumor; antiproliferative; antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200002902-A1.
 XX
 PD 20-JAN-2000.
 XX
 PF 12-JUL-1999; 99WO-US015772.
 XX
 PR 13-JUL-1998; 98US-0092647P.
 XX
 XX (GILL/) GILL P S.
 PA XX
 XX Gill PS;
 PI XX
 XX WPI; 2000-171128/15.
 DR XX
 XX Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.
 PT XX
 XX Disclosure; Page 19; 78pp; English.
 PS XX
 XX The present sequence is that of a novel peptide, derived from human saposin B, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumor activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars
 XX Sequence 7 AA;
 SQ
 Query Match 31.6%; Score 30; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 DVCQD 11
 DB 1 DVCQD 5
 RESULT 4
 AAY58697
 ID AAY58697 standard; peptide; 8 AA.
 XX
 AC AAY58697;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Antiangiogenic peptide derived from saposin B.
 XX
 KW Antiangiogenic; angiogenesis inhibitor; antitumor; antiproliferative; antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200002902-A1.
 XX
 PD 20-JAN-2000.
 XX
 PF 12-JUL-1999; 99WO-US015772.
 XX
 PR 13-JUL-1998; 98US-0092647P.
 XX
 XX (GILL/) GILL P S.
 PA XX
 XX Gill PS;
 PI XX
 XX WPI; 2000-171128/15.
 DR XX
 XX Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.
 PT XX
 XX Disclosure; Page 19; 78pp; English.
 PS XX

PA (GILL/) GILL P S.
 XX
 PI Gill PS;
 XX
 DR WPI; 2000-171128/15.
 XX
 XX Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.
 PT
 XX
 PS Disclosure; Page 19; 78pp; English.
 XX
 XX The present sequence is that of a novel peptide, derived from human saposin B, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumor activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars
 XX Sequence 8 AA;
 SQ
 Query Match 31.6%; Score 30; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 DVCQD 11
 DB 1 DVCQD 5
 RESULT 5
 AAY58696
 ID AAY58696 standard; peptide; 9 AA.
 XX
 AC AAY58696;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Antiangiogenic peptide derived from saposin B.
 XX
 KW Antiangiogenic; angiogenesis inhibitor; antitumor; antiproliferative; antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200002902-A1.
 XX
 PD 20-JAN-2000.
 XX
 PF 12-JUL-1999; 99WO-US015772.
 XX
 PR 13-JUL-1998; 98US-0092647P.
 XX
 XX (GILL/) GILL P S.
 PA
 XX
 PI Gill PS;
 XX
 XX WPI; 2000-171128/15.
 DR
 XX
 XX Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.
 PT
 XX
 PS Disclosure; Page 19; 78pp; English.
 XX

XX The present sequence is that of a novel peptide, derived from human
CC saposin B, that has antiangiogenic activity. The invention is based on
CC the discovery that saposin B (see AAY58716), previously known to be
CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
CC and antitumor activity, and also has antiproliferative and antimigratory
CC activity against endothelial cells. This activity is conserved in cryptic
CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
CC synthetically prepared and used in vitro or in vivo for the treatment of
CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
CC (claimed). The polypeptides can also be used in conjunction with
CC cytotoxic moieties to selectively kill certain cell types, e.g. for
CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
CC malformation, nonunion fracture, arthritis and other connective tissue
CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
CC corneal graft neovascularization, pyogenic granuloma, retrolental,
CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
CC vascular adhesions and hypertrophic scars
XX
SQ Sequence 9 AA;

Query Match 31.6%; Score 30; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
|
|
|
|
Db 1 DVCQD 5

RESULT 6
AAY58693
ID AAY58693 standard; peptide; 10 AA.

AC AAY58693;

XX 25-APR-2000 (first entry)

XX Antiangiogenic peptide derived from saposin B.

XX Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.

XX Homo sapiens.

XX WO200002902-A1.

XX 20-JAN-2000.

XX 12-JUL-1999; 99WO-US015772.

XX 13-JUL-1998; 98US-0092647P.

XX (GILL/) GILL P S.

XX Gill PS;

XX WPI; 2000-171128/15.

XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
PT tumor growth.

XX Disclosure; Page 19; 78pp; English.

XX The present sequence is that of a novel peptide, derived from human
CC saposin B, that has antiangiogenic activity. The invention is based on
CC the discovery that saposin B (see AAY58716), previously known to be
CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
CC and antitumor activity, and also has antiproliferative and antimigratory
CC activity against endothelial cells. This activity is conserved in cryptic
CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
CC synthetically prepared and used in vitro or in vivo for the treatment of
CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma

CC (claimed). The polypeptides can also be used in conjunction with
CC cytotoxic moieties to selectively kill certain cell types, e.g. for
CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
CC malformation, nonunion fracture, arthritis and other connective tissue
CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
CC corneal graft neovascularization, pyogenic granuloma, retrolental,
CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
CC vascular adhesions and hypertrophic scars
XX
SQ Sequence 10 AA;

Query Match 31.6%; Score 30; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
|
|
|
|
Db 1 DVCQD 5

RESULT 7

AAY58705

ID AAY58705 standard; peptide; 11 AA.

XX AC AAY58705;

XX 25-APR-2000 (first entry)

XX Antiangiogenic peptide derived from saposin B.

XX Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.

XX Synthetic.

XX Homo sapiens.

XX WO200002902-A1.

XX 20-JAN-2000.

XX 12-JUL-1999; 99WO-US015772.

XX 13-JUL-1998; 98US-0092647P.

XX (GILL/) GILL P S.

XX Gill PS;

XX WPI; 2000-171128/15.

XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
PT tumor growth.

XX Disclosure; Page 19; 78pp; English.

XX The present sequence is that of a novel peptide, based on a human saposin
CC derived peptide, that has antiangiogenic activity. The invention is
CC based on the discovery that saposin B (see AAY58716), previously known to
CC be involved in the hydrolysis of sphingolipids, has potent antiangiogenic
CC and antitumor activity, and also has antiproliferative and antimigratory
CC activity against endothelial cells. This activity is conserved in cryptic
CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
CC synthetically prepared and used in vitro or in vivo for the treatment of
CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
CC (claimed). The polypeptides can also be used in conjunction with
CC cytotoxic moieties to selectively kill certain cell types, e.g. for
CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
CC malformation, nonunion fracture, arthritis and other connective tissue
CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
CC corneal graft neovascularization, pyogenic granuloma, retrolental,
CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
CC vascular adhesions and hypertrophic scars
XX

SQ Sequence 11 AA;

Query Match 31.6%; Score 30; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DVCQD 11
 |||||
 DB 2 DVCQD 6

RESULT 8

AAV58691
 ID AAV58691 standard; peptide; 11 AA.

XX AC AAV58691;

XX DT 25-APR-2000 (first entry)

XX DE Antiangiogenic peptide derived from saposin B.

XX KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
 XX KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.

XX OS Homo sapiens.

XX PN WO200002902-A1.

XX PD 20-JAN-2000.

XX PF 12-JUL-1999; 99WO-US015772.

XX PR 13-JUL-1999; 98US-0092647P.

XX PA (GILL/) GILL P S.

XX PI Gill PS;

XX DR WPI; 2000-171128/15.

XX PT Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.

XX PS Claim 23; Page 59; 78pp; English.

XX CC The present sequence is that of a claimed peptide, derived from human saposin B, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAV58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumour activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAV58694-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars

SQ Sequence 11 AA;

Query Match 31.6%; Score 30; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DVCQD 11
 |||||
 DB 2 DVCQD 6

RESULT 10

AAV58685

ID AAV58685 standard; peptide; 15 AA.

XX AC AAV58685;

XX DT 25-APR-2000 (first entry)

XX DE Antiangiogenic peptide derived from saposin B.

XX KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;

RESULT 9

AAW18587

ID AAW18587 standard; peptide; 15 AA.

XX AC AAW18587;

XX DT 01-FEB-1998 (first entry)

XX DE Universal primary sperm-egg binding protein inactive fragment.

XX KW Universal primary sperm-egg binding protein; UPSEBP; fertility; contraceptive.

XX OS Synthetic.

XX PN WO9725620-A1.

XX PD 17-JUL-1997.

XX PF 06-JAN-1997; 97WO-US000105.

XX PR 11-JAN-1996; 96US-00584671.

XX PA (PENN-) PENN STATE RES FOUND.

XX PI Hammerstedt RH, Cramer PG, Barbato GF;

XX DR WPI; 1997-373003/34.

XX PT Protein providing for initial binding of sperm to oocyte investment(s) - used for enhancing sperm binding, contraception and determining the number of sperm binding sites on an oocyte investment.

XX PS Disclosure; Page 29; 46pp; English.

XX CC A synthetic peptide (see AAW18581) provides sperm binding capability similar to that of universal primary sperm-egg binding protein (UPSEBP). UPSEBP was originally isolated from rooster sperm. It provides for initial bonding of sperm to oocyte investments and has biological activity in a variety of avian and mammalian species. A shorter amino acid sequence (AAW18586) of the synthetic peptide is devoid of binding capability, and addition of amino acids distal to the N-terminal Asn residue of this short peptide (AAW18587 and AAW18588) did not substantially alter biological activity. Native or synthetic UPSEBPs can be used in claimed methods for enhancing sperm-egg binding, particularly of thawed cryopreserved sperm, for determining the fertilisation potential of sperm, and for determining the number of sperm binding sites on an egg investment. Analogues of the polypeptides that bind sperm but not oocytes can be used as contraceptives

SQ Sequence 15 AA;

Query Match 31.6%; Score 30; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DVCQD 11
 |||||
 DB 9 DVCQD 13

KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX Synthetic.
 OS Homo sapiens.
 XX WO200002902-A1.
 XX PD 20-JAN-2000.
 XX PF 12-JUL-1999; 99WO-US015772.
 XX PR 13-JUL-1998; 98US-0092647P.
 XX XX (GILL/) GILL P S.
 PA Gill PS;
 PI WPI; 2000-171128/15.
 DR Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.
 PT Disclosure; Page 19; 78pp; English.
 XX The present sequence is that of a novel peptide, based on a human saposin B derived peptide, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumour activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (Claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders. Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars

Sequence 15 AA;
 Query Match 31.6%; Score 30; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 76; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;
 OY 7 DVCQD 11
 DB 7 DVCQD 11
 |||||
 |||||

RESULT 11
 AAW18588
 ID AAW18588 standard; peptide; 19 AA.
 XX AAW18588;
 AC AAW18588;
 XX 01-FEB-1998 (first entry)
 XX Universal primary sperm-egg binding protein inactive fragment.
 XX Universal primary sperm-egg binding protein; UPSEBP; fertility; contraceptive.
 KW Synthetic.
 XX WO9725620-A1.
 XX PN 17-JUL-1997.
 XX PD 06-JAN-1997; 97WO-US000105.

XX 11-JAN-1996; 96US-00584671.
 XX (PENN-) PENN STATE RES FOUND.
 XX Hammerstedt RH, Cramer PG, Barbato GF;
 XX WPI; 1997-373003/34.
 DR Protein providing for initial binding of sperm to oocyte investment(s) -
 XX used for enhancing sperm binding, contraception and determining the
 XX number of sperm binding sites on an oocyte investment.
 PS Disclosure; Page 29; 46pp; English.
 XX A synthetic peptide (see AAW18581) provides sperm binding capability
 CC similar to that of universal primary sperm-egg binding protein (UPSEBP).
 CC UPSEBP was originally isolated from rooster sperm. It provides for
 CC initial bonding of sperm to oocyte investments and has biological
 CC activity in a variety of avian and mammalian species. A shorter amino
 CC acid sequence (AAW18586) of the synthetic peptide is devoid of binding
 CC capability, and addition of amino acids distal to the N-terminal Asn
 CC residue of this short peptide (AAW18587 and AAW18588) did not
 CC substantially alter biological activity. Native or synthetic UPSEBPs can
 CC be used in claimed methods for enhancing sperm-egg binding, particularly
 CC of thawed cryopreserved sperm, for determining the fertilisation
 CC potential of sperm, and for determining the number of sperm binding
 CC binding sites on an egg investment. Analogues of the polypeptides that
 CC bind sperm but not oocytes can be used as contraceptives

Sequence 19 AA;
 Query Match 31.6%; Score 30; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 94; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;
 OY 7 DVCQD 11
 DB 8 DVCQD 12
 |||||
 |||||

RESULT 12
 AAY58708
 ID AAY58708 standard; peptide; 5 AA.
 XX AAY58708;
 AC AAY58708;
 XX 25-APR-2000 (first entry)
 DT Antiangiogenic peptide derived from saposin B.
 XX Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
 KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX Synthetic.
 OS Homo sapiens.
 XX WO200002902-A1.
 XX PN 20-JAN-2000.
 XX 12-JUL-1999; 99WO-US015772.
 XX 13-JUL-1998; 98US-0092647P.
 XX (GILL/) GILL P S.
 PA Gill PS;
 PI WPI; 2000-171128/15.
 DR Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.
 PT Disclosure; Page 29; 46pp; English.

XX Disclosure; Page 19; 78pp; English.
 XX The present sequence is that of a novel peptide, based on a human saposin B derived peptide, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumor activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars
 XX Sequence 5 AA;

Query Match 30.5%; Score 29; DB 3; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 7 DVCQD 11
 I:||||
 Db 1 DICQD 5

RESULT 13
 AAY58709
 ID AAY58709 standard; peptide; 5 AA.
 AC AAY58709;
 XX
 XX 25-APR-2000 (first entry)
 XX Antiangiogenic peptide derived from saposin B.
 DE Antiangiogenic; angiogenesis inhibitor; antitumor; antiproliferative;
 XX Antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 KW Synthetic.
 XX Homo sapiens.
 OS WO200002902-A1.
 XX 20-JAN-2000.
 PD 12-JUL-1999; 99WO-US015772.
 PF 13-JUL-1998; 98US-0092647P.
 PR (GILL/) GILL P S.
 PA Gill PS;
 PI WPI; 2000-171128/15.
 XX Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.
 PS Disclosure; Page 19; 78pp; English.

XX The present sequence is that of a novel peptide, based on a human saposin B derived peptide, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumor activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic

CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars
 XX Sequence 5 AA;

Query Match 28.4%; Score 27; DB 3; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 7 DVCQD 11
 I:||||
 Db 1 DICQD 5

RESULT 14
 AAY58711
 ID AAY58711 standard; peptide; 5 AA.
 AC AAY58711;
 XX
 XX 25-APR-2000 (first entry)
 XX Antiangiogenic peptide derived from saposin B.
 DE Antiangiogenic; angiogenesis inhibitor; antitumor; antiproliferative;
 XX Antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 KW Synthetic.
 XX Homo sapiens.
 OS WO200002902-A1.
 XX 20-JAN-2000.
 PD 12-JUL-1999; 99WO-US015772.
 PF 13-JUL-1998; 98US-0092647P.
 PR (GILL/) GILL P S.
 PA Gill PS;
 PI WPI; 2000-171128/15.
 XX Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.
 PS Disclosure; Page 19; 78pp; English.

XX The present sequence is that of a novel peptide, based on a human saposin B derived peptide, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumor activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental

CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
 CC vascular adhesions and hypertrophic scars
 XX
 SQ Sequence 5 AA;

Query Match 28.4%; Score 27; DB 3; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
 Db 1 DVCED 5

RESULT 15
 ABP71131
 ID ABP71131 standard; protein; 40 AA.
 XX
 AC ABP71131;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE E10 CARD protein fragment.
 XX
 KW BTF3; cell death; apoptosis; basic transcription factor; cytostatic;
 KW neurotropic; neuroprotective; antiparkinsonian; antiarteriosclerotic;
 KW antirheumatic; antiarthritic; gene therapy; CARD; E10.
 XX
 OS Unidentified.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 34 /note= "unknown"
 FT
 XX WO200295001-A2.
 XX
 XX 28-NOV-2002.
 XX
 XX 21-MAY-2002; 2002WO-US016230.
 XX
 XX 21-MAY-2001; 2001US-0292559P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 XX
 PI Rothman JH, Bloss T, Witze E;
 XX
 PI WPI; 2003-167228/16.
 DR
 XX
 XX Inhibiting or increasing programmed cell death of a cell, for treating
 PT e.g. cancer, comprises upregulating or inhibiting, respectively, the
 PT expression or activity of basic transcription factor (BTF)3 or its
 PT homolog in the cell.
 XX
 XX Example; Fig 2B; 84pp; English.
 PS
 XX The invention relates to inhibiting or increasing programmed cell death
 CC of a cell. The method involves upregulating or inhibiting, respectively,
 CC the expression or activity of basic transcription factor (BTF)3 or its
 CC homolog in the cell. The BTF3 polypeptides and nucleic acids are useful
 CC for inhibiting or increasing programmed cell death. They are used for
 CC screening for an agent that increases or inhibits programmed cell death
 CC or pre-screening for an agent that modulates programmed cell death. The
 CC screened agent that increases or inhibits programmed cell death, is used
 CC for diagnosing or treating cancer or neurodegenerative diseases (e.g.
 CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease
 CC or multiple sclerosis), atherosclerosis, or rheumatoid arthritis.
 CC Sequences ABP71124-135 represent peptide fragments various CARD proteins
 XX
 SQ Sequence 40 AA;

Query Match 28.4%; Score 27; DB 6; Length 40;
 Best Local Similarity 80.0%; Pred. No. 6.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11
 Db 12 DMCQD 16

RESULT 16
 ADS05060
 ID ADS05060 standard; protein; 40 AA.
 XX
 AC ADS05060;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Staphylococcus epidermis polypeptide seqid 4355.
 XX
 KW antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;
 KW recombinant expression vector; infection; computer readable medium;
 KW computer based system.
 XX
 OS Staphylococcus epidermidis.
 XX
 FN US2004147734-A1.
 XX
 PD 29-JUL-2004.
 XX
 PF 01-DEC-2003; 2003US-00724972.
 XX
 PR 08-NOV-1997; 97US-0064964P.
 PR 13-AUG-1998; 98US-00134001.
 PR 29-NOV-1999; 99US-00450969.
 XX
 PA (DOUC/) DOUCETTB-STAMM L.
 PA (BUSH/) BUSH D.
 XX
 PI Doucette-Stamm L, Bush D;
 XX
 WPI; 2004-580138/56.
 DR N-PSDB; ADS01288.
 DR
 XX New isolated polypeptide and encoding nucleic acid derived from
 PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or
 PT treating an S. epidermidis bacterial infection.
 XX
 PS Claim 17; SEQ ID NO 4355; 741pp; English.
 XX
 CC The invention describes an isolated nucleic acid comprising a nucleotide
 CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:
 CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any
 CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as
 CC given in the specification. Also described are: a recombinant expression
 CC vector; a cell comprising a recombinant expression vector of (1);
 CC producing an S. epidermidis polypeptide; an isolated nucleic acid
 CC comprising a nucleotide sequence of at least 8 nucleotides in length; a
 CC vaccine composition for prevention or treatment of an S. epidermidis
 CC infection, comprising a nucleic acid cited above and a carrier; treating
 CC a subject for S. epidermidis infection; a recombinant or substantially
 CC pure preparation of an S. epidermidis polypeptide or its fragment; a
 CC vaccine composition for prevention or treatment of an S. epidermidis
 CC infection; detecting the presence of a Staphylococcus nucleic acid in a
 CC sample; a computer readable medium having recorded in it the nucleotide
 CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based
 CC system for identifying fragments of the Staphylococcus genome of
 CC commercial importance; a computer based system for identifying fragments
 CC of the Staphylococcus plasmids of commercial importance; identifying
 CC commercially important nucleic acid fragments of the Staphylococcus
 CC genome and/or plasmids; and identifying an expression modulating fragment
 CC of the Staphylococcus genome and/or plasmids. The methods and
 CC compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of an Staphylococcus epidermidis bacterial
 CC infection. This is the amino acid sequence of a S. epidermidis protein of
 CC the invention.
 CC

SQ Sequence 40 AA;

Query Match 28.4%; Score 27; DB 8; Length 40;
 Best Local Similarity 80.0%; Pred. No. 6.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 DVCQD 11
 12 DMCQD 16

Db 12 DMCQD 16

RESULT 17
 ADB47923
 ID ADB47923 standard; protein; 48 AA.

XX AC ADB47923;
 XX DT 04-DEC-2003 (first entry)
 XX DE Novel human secreted protein associated polypeptide #2.

XX KW human; secreted protein; insulin; haemoglobin S; haemoglobin B;
 KW superoxide; SOD; catalase; DNA repair protein; oncogene;
 KW tumour suppressor; tumour necrosis factor; TNF; inflammation;
 KW blood vessel growth inhibition; immune response; immune system disorder;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW peripheral artery disease; limb ischaemia; arterio-arterial fistula;
 KW arteriovenous fistula; congenital heart defect;
 KW neovascularisation disorder; wound healing;
 KW epithelial cell proliferation; neurological disease; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; mania; dementia;
 KW infectious disease.

XX OS Homo sapiens.
 XX PN US2003054443-A1.
 XX PD 20-MAR-2003.

XX PF 04-OCT-2001; 2001US-00969730.

XX PR 05-AUG-1997; 97US-0054798P.
 PR 05-AUG-1997; 97US-0054803P.
 PR 05-AUG-1997; 97US-0054804P.
 PR 05-AUG-1997; 97US-0054806P.
 PR 05-AUG-1997; 97US-0054807P.
 PR 05-AUG-1997; 97US-0054808P.
 PR 05-AUG-1997; 97US-0054809P.
 PR 05-AUG-1997; 97US-0055303P.
 PR 05-AUG-1997; 97US-0055310P.
 PR 05-AUG-1997; 97US-0055311P.
 PR 05-AUG-1997; 97US-0055312P.
 PR 05-AUG-1997; 97US-0055386P.
 PR 18-AUG-1997; 97US-0055970P.
 PR 18-AUG-1997; 97US-0055986P.
 PR 19-AUG-1997; 97US-0056364P.
 PR 19-AUG-1997; 97US-0056365P.
 PR 19-AUG-1997; 97US-0056366P.
 PR 19-AUG-1997; 97US-0056367P.
 PR 19-AUG-1997; 97US-0056370P.
 PR 19-AUG-1997; 97US-0056371P.
 PR 19-AUG-1997; 97US-0056557P.
 PR 19-AUG-1997; 97US-0056563P.
 PR 19-AUG-1997; 97US-0056731P.
 PR 19-AUG-1997; 97US-0056732P.
 PR 04-AUG-1998; 98WO-US016235.
 PR 04-FEB-1999; 99US-0024411P.
 PR 06-OCT-2000; 2000US-0238291P.
 PR 01-FEB-2001; 2001US-00774639.

XX PA (RUBE/) RUBEN S M.
 PA (SOPP/) SOPPET D R.
 PA (EBNE/) EBNER R.

PA (OLSE/) OLSEN H S.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (YUGG/) YU G.
 PA (NLJJ/) NI J.
 PA (ROSE/) ROSEN C A.
 PA (BREW/) BREWER L A.
 PA (JANA/) JANAT F.
 PA (BIRS/) BIRSE C E.

XX Ruben SM, Soppet DR, Ebner R, Olsen HS, Young PE, Greene JM,
 PI Ferrie AM, Yu G, Ni J, Rosen CA, Brewer LA, Janat F, Birse CE;
 XX WPI; 2003-695903/66.

XX Novel human secreted proteins useful for treating and/or diagnosing
 PT disorders of immune system, cardiovascular disorders such as peripheral
 PT artery disease, neurological diseases such as Alzheimer's disease.

XX Disclosure; Page 4; 333pp; English.

XX The invention relates to novel human secreted proteins. The protein is
 CC useful for preventing, treating or ameliorating a medical condition. The
 CC protein is useful for diagnosing a pathological condition or
 CC susceptibility to a pathological condition in a subject. The protein is
 CC useful for identifying a binding partner. The nucleic acid is useful for
 CC diagnosing pathological condition or a susceptibility to pathological
 CC condition in a subject. The protein is useful as reagents for
 CC differential identification of the tissues or cell types present in a
 CC biological sample. The protein can be administered to patients having
 CC absent or decreased levels of polypeptides e.g. insulin, to supplement
 CC absent or decreased levels of different polypeptides, e.g. haemoglobin S
 CC for haemoglobin B, superoxide (SOD), catalase, DNA repair protein, to
 CC inhibit the activity of a polypeptide e.g. an oncogene or tumour
 CC suppressor, to activate the activity of polypeptide e.g. by binding to a
 CC receptor, to reduce the activity of membrane bound receptor by competing
 CC with it for free ligand e.g. soluble tumour necrosis factor (TNF)
 CC receptors used in reducing inflammation, or to bring about a desired
 CC response e.g. blood vessel growth inhibition, enhancement of immune
 CC acid are useful for treating, preventing, detecting, diagnosing disorders
 CC of immune system involving abnormal growth of specific types of cells as
 CC well as of other cell types where expression has been observed. The
 CC protein, the nucleic acid and antibodies are useful for treating,
 CC preventing and/or diagnosing diseases, disorders and/or conditions of
 CC immune system, hyperproliferative disorders including neoplasms,
 CC cardiovascular disorders (such as peripheral artery disease, limb
 CC ischaemia, arterio-arterial fistula, arteriovenous fistula, congenital
 CC heart defects, etc), neovascularisation disorders, wound healing and
 CC epithelial cell proliferation, neurological diseases (such as Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease, mania, dementia,
 CC etc), infectious diseases caused by virus, bacteria, fungi, etc. The
 CC present sequence represents the amino acid sequence of a novel human
 CC secreted protein associated polypeptide.

XX SQ Sequence 48 AA;

Query Match 28.4%; Score 27; DB 7; Length 48;
 Best Local Similarity 80.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 DVCQD 11
 28 DMCQD 32

Db 28 DMCQD 32

RESULT 18
 ID ADJ55478
 ADJ55478 standard; protein; 48 AA.

XX AC ADJ55478;
 XX XX

DT 06-MAY-2004 (first entry)

XX Novel human secreted protein fragment #2.

XX neuroprotective; neurotropic; antiparkinsonian; anticonvulsant;

XX antidabetic; antirheumatic; antiarthritic; dermatological;

KW antinflammatory; immunosuppressive; antithyroid; antianaemic;

KW vasotropic; anti-HIV; hepatotropic; virucide; antibacterial; fungicide;

KW antiparasitic; muscular; gynaecological; gastrointestinal; respiratory;

KW cardiovascular; antiarteriosclerotic; antiarrhythmic; cardiac;

KW nephrologic; litholytic; cytostatic; gene therapy; neural disorder;

KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;

KW amyotrophic lateral sclerosis; multiple sclerosis;

KW immune system disorder; diabetes; rheumatoid arthritis;

KW systemic lupus erythematosus; autoimmune thyroiditis; haemolytic anaemia;

KW inflammatory disorder; ischaemia-reperfusion injury;

KW inflammatory bowel disease; Crohn's disease; infectious disease;

KW infection; muscular disorder; reproductive disorder;

KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;

KW atherosclerosis; arrhythmia; myocarditis; renal disorder;

KW acute glomerulonephritis; pyelonephritis; renal lithiasis;

KW hyperproliferative disorder; cancer; human.

XX Homo sapiens.

OS

XX US2004023283-A1.

XX 05-FEB-2004.

XX

PF 18-JUL-2003; 2003US-00621363.

XX

PR 05-AUG-1997; 97US-0054798P.

PR 05-AUG-1997; 97US-0054803P.

PR 05-AUG-1997; 97US-0054804P.

PR 05-AUG-1997; 97US-0054806P.

PR 05-AUG-1997; 97US-0054807P.

PR 05-AUG-1997; 97US-0054808P.

PR 05-AUG-1997; 97US-0054809P.

PR 05-AUG-1997; 97US-0055309P.

PR 05-AUG-1997; 97US-0055310P.

PR 05-AUG-1997; 97US-0055311P.

PR 05-AUG-1997; 97US-0055312P.

PR 05-AUG-1997; 97US-0055386P.

PR 18-AUG-1997; 97US-0055970P.

PR 18-AUG-1997; 97US-0055986P.

PR 19-AUG-1997; 97US-0056364P.

PR 19-AUG-1997; 97US-0056365P.

PR 19-AUG-1997; 97US-0056366P.

PR 19-AUG-1997; 97US-0056367P.

PR 19-AUG-1997; 97US-0056370P.

PR 19-AUG-1997; 97US-0056371P.

PR 19-AUG-1997; 97US-0056557P.

PR 19-AUG-1997; 97US-0056563P.

PR 19-AUG-1997; 97US-0056731P.

PR 19-AUG-1997; 97US-0056732P.

PR 04-AUG-1998; 98WO-US016235.

PR 04-FEB-1999; 99US-00244112.

PR 06-OCT-2000; 2000US-0238291P.

PR 01-FEB-2001; 2001US-00774639.

PR 04-OCT-2001; 2001US-00969730.

XX (HUMA-) HUMAN GENOME SCI INC.

XX

PI Ruben SM, Soppet DR, Ebner R, Olsen HS, Young PE, Greene JM;

PI Ferrie AM, Yu G, Ni J, Rosen CA, Brewer L, Janat F, Birse CE;

XX WPI; 2004-142651/14.

XX New human secreted proteins and nucleic acid molecules, useful for

PT detecting, preventing, diagnosing, treating or ameliorating medical

PT conditions, e.g. immune system disorders, reproductive disorders or

XX infectious diseases.

PS Disclosure; SEQ ID NO 206; 333pp; English.

XX

CC The invention describes an isolated, secreted polypeptide comprising an

CC amino acid sequence at least 95% identical to: a polypeptide fragment,

CC domain or epitope, a full-length protein, or a secreted form of any one

CC of 97 sequences of 8-457 amino acids (I), given in the specification, or

CC the encoded sequence included in any one of the American Type Culture

CC Collection (ATCC) deposit numbers (II) given in the specification; a

CC polypeptide fragment of (I), or the encoded sequence included in (II),

CC having biological activity; or a variant, allelic variant, or a species

CC homologue of (I). The polypeptides, nucleic acid molecules and antibodies

CC are useful for detecting, preventing, diagnosing, prognosticating,

CC treating or ameliorating medical conditions such as neural disorders,

CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's chorea,

CC amyotrophic lateral sclerosis or multiple sclerosis, immune system

CC disorders, e.g. diabetes, rheumatoid arthritis, systemic lupus

CC erythematosus, autoimmune thyroiditis or haemolytic anaemia, inflammatory

CC disorders, e.g. ischaemia-reperfusion injury, inflammatory bowel disease

CC or Crohn's disease, infectious diseases such as HIV infection, hepatitis

CC infection, bacterial infection, fungal infection or parasitic infection,

CC muscular disorders, reproductive disorders, gastrointestinal disorders,

CC pulmonary disorders, cardiovascular disorders, e.g. atherosclerosis,

CC arrhythmia or myocarditis, renal disorders, e.g. acute

CC glomerulonephritis, pyelonephritis or renal lithiasis, hyperproliferative

CC disorders, or cancerous diseases or conditions. The nucleic acids are

CC also useful for chromosome identification, radiation hybrid mapping or

CC long-range restriction mapping, as molecular weight markers, or as

CC hybridisation or diagnostic probes. This is the amino acid sequence of a

XX novel human secreted protein fragment.

SQ Sequence 48 AA;

Query Match 28.4%; Score 27; DB 8; Length 48;

Best Local Similarity 80.0%; Pred. No. 7.8e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 11

Db 28 DLQCD 32

|||

|||

RESULT 19

AA17684

ID AA17684 standard; protein; 55 AA.

XX

XX AA17684;

AC

XX

DT 12-OCT-2001 (first entry)

XX

DE Peptide #4118 encoded by probe for measuring cervical gene expression.

XX

KW Probe; human; microarray; gene expression; cervical epithelial cell;

KW cervical cancer.

XX

OS Homo sapiens.

XX

XX WO200157278-A2.

PN

XX

PD 09-AUG-2001.

XX

XX

PF 30-JAN-2001; 2001WO-US0000670.

XX

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

XX

PI

XX WPI; 2001-488901/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.
XX
XX Claim 27; SEQ ID NO 22510; 487pp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
CC (SENPs: see AA110068-AA128459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 55 AA;
SQ

Query Match 28.4%; Score 27; DB 4; Length 55;
Best Local Similarity 80.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 7 DVCOD 11
Db 32 DVCED 36
|||||

RESULT 20
ABB36706
ID ABB36706 standard; peptide; 55 AA.
XX
XX ABB36706;
XX
XX 04-FEB-2002 (first entry)
XX
XX Peptide #4212 encoded by human foetal liver single exon probe.
XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX Homo sapiens.
XX WO200157277-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
XX Claim 27; SEQ ID NO 29341; 639pp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The

CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 55 AA;
SQ

Query Match 28.4%; Score 27; DB 4; Length 55;
Best Local Similarity 80.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 7 DVCOD 11
Db 32 DVCED 36
|||||

RESULT 21
AAM30198
ID AAM30198 standard; protein; 55 AA.
XX
XX AAM30198;
XX
XX 17-OCT-2001 (first entry)
XX
XX Peptide #4235 encoded by probe for measuring placental gene expression.
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX Homo sapiens.
XX
XX WO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 30467; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENPs:
CC see AA131315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX Sequence 55 AA;
SQ

Query Match 28.4%; Score 27; DB 4; Length 55;
Best Local Similarity 80.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 7 DVCOD 11
Db 32 DVCED 36
|||||

```
RESULT 22
ABB31493
ID ABB31493 standard; peptide; 55 AA.
XX
AC ABB31493;
XX
DT
XX
XX 01-FEB-2002 (first entry)
XX
DE Peptide #4144 encoded by breast cell single exon nucleic acid probe.
XX
XX Human; microarray; single exon probe; gene expression; breast; disease;
KW cancer.
XX
KW Homo sapiens.
XX
OS
XX
XX WO200157271-A2.
FN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000662.
PF
XX
XX 04-FEB-2000; 2000US-0180312P.
PR
XX 26-MAY-2000; 2000US-0207456P.
PR
XX 30-JUN-2000; 2000US-00608408.
PR
XX 03-AUG-2000; 2000US-00632366.
PR
XX 21-SEP-2000; 2000US-0234687P.
PR
XX 27-SEP-2000; 2000US-0236359P.
PR
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
FA
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX
XX WPI; 2001-496933/54.
DR
XX
XX New spatially-addressable set of single exon nucleic acid probes, useful
PT for measuring gene expression in sample derived from human breast,
PT comprises number of single exon nucleic acid probes.
XX
XX Claim 27; SEQ ID NO 14461; 327pp + Sequence Listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting the
CC probes with a collection of detectably labelled nucleic acids derived
CC from mRNA of human breast, and then measuring the label bound to each
CC probe of the microarray. The probes are useful for verifying the
CC expression of regions of genomic DNA predicted to encode proteins. They
CC are useful for gene discovery, and for determining predisposition and/or
CC prognosing breast disease. Gene expression analysis is useful for
CC assessing the toxicity of chemical agents on cells. The microarray of
CC this invention presents a far greater diversity of probes for measuring
CC gene expression, with far less bias than expressed sequence tag
CC microarrays. The method is suitable for rapid production of functional
CC information from genomic sequence. The present sequence is a peptide
CC encoded by a single exon nucleic acid probe of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 55 AA;

Query Match 28.4%; Score 27; DB 4; Length 55;
Best Local Similarity 80.0%; Pred. NO. 8.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 7 DVCOD 11
Db 32 DVCED 36

RESULT 23
ABB31493
ID ABB31493 standard; peptide; 55 AA.
XX
AC ABB31493;
XX
DT
XX
XX 01-FEB-2002 (first entry)
XX
DE Peptide #4144 encoded by breast cell single exon nucleic acid probe.
XX
XX Human; microarray; single exon probe; gene expression; breast; disease;
KW cancer.
XX
KW Homo sapiens.
XX
OS
XX
XX WO200157271-A2.
FN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000662.
PF
XX
XX 04-FEB-2000; 2000US-0180312P.
PR
XX 26-MAY-2000; 2000US-0207456P.
PR
XX 30-JUN-2000; 2000US-00608408.
PR
XX 03-AUG-2000; 2000US-00632366.
PR
XX 21-SEP-2000; 2000US-0234687P.
PR
XX 27-SEP-2000; 2000US-0236359P.
PR
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
FA
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX
XX WPI; 2001-488899/53.
DR
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
PT
XX Claim 15; SEQ ID NO 23809; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABAA1305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 55 AA;

Query Match 28.4%; Score 27; DB 4; Length 55;
Best Local Similarity 80.0%; Pred. NO. 8.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 7 DVCOD 11
Db 32 DVCED 36

RESULT 24
AAM69858
ID AAM69858 standard; protein; 55 AA.
XX
AC AAM69858;
XX
XX 06-NOV-2001 (first entry)
DT
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30164.
```

```
XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
XX Homo sapiens.
XX WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
XX PS Example 4; SEQ ID NO 30164; 658pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukaemia and myeloma. The present sequence is a
XX protein encoded by one of the probes of the invention
XX SQ Sequence 55 AA;
    Query Match      28.4%; Score 27; DB 4; Length 55;
    Best Local Similarity 80.0%; Pred. No. 8.8e+02;
    Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 7 DVCQD 11
DB 32 DVCED 36
    |||:|
    |||:|

RESULT 25
AAM57463
ID AAM57463 standard; protein; 55 AA.
XX
XX AAM57463;
XX
XX 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 29568.
XX DE Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
XX Homo sapiens.
XX OS
XX WO200157275-A2.
XX PN
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
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PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX DR Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains.
XX PS Example 4; SEQ ID NO 29568; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention
XX SQ Sequence 55 AA;
    Query Match      28.4%; Score 27; DB 4; Length 55;
    Best Local Similarity 80.0%; Pred. No. 8.8e+02;
    Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 7 DVCQD 11
DB 32 DVCED 36
    |||:|
    |||:|

Search completed: June 30, 2005, 11:52:57
Job time : 201.765 secs
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: June 30, 2005, 11:46:17 ; Search time 190.123 Seconds

(without alignments)

188.538 Million cell updates/sec

Title: US-09-743-684A-45

Perfect score: 95

Sequence: 1 XXXXXDVQDXXXXXXXXXXXXXXX.....XXXXXXXXXXXXXXXXXXXXX 70

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 132411

Minimum DB seq length: 0

Maximum DB seq length: 71

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	25	26.3	37 2 Q72XM4	Q72xm4 bacillus ce
2	25	26.3	46 2 Q80V51	Q80v51 mus musculus
3	25	26.3	50 2 Q716L2	Q716l2 mycobacteri
4	25	26.3	53 2 Q8R194	Q8r194 mus musculus
5	25	26.3	61 2 Q87SC2	Q87sc2 vibrio para
6	25	26.3	66 2 Q8SBL8	Q8sbl8 bacterioph
7	24	25.3	31 2 Q18888	Q18888 canis fami
8	24	25.3	37 1 ME20_EUPRA	P26888 euploetes ra
9	24	25.3	37 2 Q6T3W6	Q6t3w6 heliconius
10	24	25.3	38 2 Q8DXU1	Q8dxu1 streptococc
11	24	25.3	38 2 Q9DE17	Q9de17 gallus gall
12	24	25.3	39 2 Q6ZVI9	Q6zvi9 bacillus li
13	24	25.3	39 2 Q9DE18	Q9de18 gallus gall
14	24	25.3	42 2 Q732A2	Q732a2 bacillus ce
15	24	25.3	42 2 Q819L0	Q819l0 bacillus ce
16	24	25.3	42 2 Q81MR8	Q81mr8 bacillus an
17	24	25.3	46 2 Q9P0Z7	Q9p0z7 homo sapien
18	24	25.3	48 1 R332_MYCCE	Q9zb82 mycoplasma
19	24	25.3	48 1 R332_MYCPN	P56850 mycoplasma
20	24	25.3	52 2 Q65RJ4	Q65rj4 manheimia
21	24	25.3	53 2 Q8RYU2	Q8ryu2 oryza sativ
22	24	25.3	54 2 Q9U7K6	Q9u7k6 plasmodium
23	24	25.3	54 2 Q6L9F5	Q6l9f5 heliobacill
24	24	25.3	54 2 Q9PDP0	Q9pdp0 xylella fas
25	24	25.3	55 2 Q9BMS4	Q9bms4 plasmodium
26	24	25.3	55 2 Q9U7G1	Q9u7g1 plasmodium
27	24	25.3	56 1 IBB1_WHEAT	P09863 triticum ae
28	24	25.3	56 2 Q6PD47	Q6pda7 homo sapien
29	24	25.3	58 2 Q74FP9	Q74fp9 geobacter s
30	24	25.3	59 2 Q8WZ24	Q8wz24 plasmodium
31	24	25.3	59 2 Q8BJH0	Q8bjh0 plasmodium

32	24	25.3	63 2 Q8N6W4	Q8n6w4 homo sapien
33	24	25.3	68 2 Q9JWL2	Q9jwl2 neisseria m
34	24	25.3	68 2 Q8VBV2	Q8vbv2 rattus norv
35	24	25.3	69 2 Q708N1	Q708n1 bacterioph
36	24	25.3	69 2 Q8K4N2	Q8k4n2 mus musculu
37	24	25.3	70 2 Q9ND04	Q9nd04 plasmodium
38	24	25.3	70 2 Q9ND25	Q9nd25 plasmodium
39	24	25.3	71 2 Q9ND05	Q9nd05 plasmodium
40	24	25.3	71 2 Q9ND35	Q9nd35 plasmodium
41	24	25.3	71 2 Q9ND36	Q9nd36 plasmodium
42	23	24.2	20 1 TXV2_PHONI	Q9tws5 phoneutria
43	23	24.2	29 2 Q9FZX6	Q9fzx6 bacterioph
44	23	24.2	43 2 Q51033	Q51033 borrelia bu
45	23	24.2	44 2 Q86GH7	Q86gh7 drosophila
46	23	24.2	49 2 Q7MRV0	Q7mrvo wolinnella s
47	23	24.2	52 2 Q97894	Q97894 human immun
48	23	24.2	53 2 Q7UQZ4	Q7uqz4 rhodopirell
49	23	24.2	57 2 Q95MD7	Q95md7 bos taurus
50	23	24.2	58 1 RHO_THIFE	P52158 thiobacillu
51	23	24.2	59 2 Q80J11	Q80j11 ruminant cy
52	23	24.2	59 2 Q9DQC9	Q9dq9 caprine her
53	23	24.2	60 2 Q6MAL3	Q6mal3 parachlamyd
54	23	24.2	61 2 Q8YVZ8	Q8yvz8 anabaena sp
55	23	24.2	61 2 Q73PC3	Q73pc3 treponema d
56	23	24.2	62 2 Q61JK8	Q61jk8 drosophila
57	23	24.2	63 2 Q8BMZ2	Q8bmz2 mus musculu
58	23	24.2	64 2 Q711D2	Q711j2 lactobacill
59	23	24.2	66 2 Q8ZZW4	Q8zzw4 pyrobaculum
60	23	24.2	66 2 Q6EUW0	Q6euw0 rattus norv
61	23	24.2	67 1 IBB2_SETIT	P19860 setaria ita
62	23	24.2	67 1 IBB3_SETIT	P22737 setaria ita
63	23	24.2	69 2 Q9VZQ5	Q9vzq5 drosophila
64	23	24.2	69 2 Q6V7V9	Q6v7v9 gallus gall
65	23	24.2	69 2 Q6V7V9	Q6v7v9 gallus gall
66	23	24.2	70 2 Q6KGE2	Q6kge2 bacterioph
67	23	24.2	70 2 Q42236	Q42236 arabidopsis
68	22	23.2	44 2 Q86814	Q86814 skeletonema
69	22	23.2	51 2 Q8MVR3	Q8mvr3 trypanosoma
70	22	23.2	54 2 Q6RA82	Q6ra82 homo sapien
71	22	23.2	54 2 Q8C7R8	Q8c7r8 mus musculu
72	22	23.2	55 2 Q98JCB	Q98jcb rhizobium l
73	22	23.2	58 2 Q6KGN6	Q6kgn6 bacterioph
74	22	23.2	63 2 Q8NGQ7	Q8ngq7 corynebacte
75	22	23.2	64 1 IBB1_COILA	P07679 coix lachry
76	22	23.2	66 2 Q6ZGM8	Q6zgm8 oryza sativ
77	22	23.2	68 2 Q6GZW2	Q6gzw2 frog virus
78	21	22.1	24 2 Q13660	Q13660 homo sapien
79	21	22.1	24 2 Q13661	Q13661 homo sapien
80	21	22.1	24 2 Q9NQY3	Q9nqy3 homo sapien
81	21	22.1	31 2 Q9BXM4	Q9bxm4 homo sapien
82	21	22.1	32 2 Q72HE5	Q72he5 thermus the
83	21	22.1	32 2 Q81885	Q81885 human papil
84	21	22.1	34 1 VSTX_GRASP	P60980 grammoetola
85	21	22.1	35 2 Q6QNA6	Q6qna6 homo sapien
86	21	22.1	35 2 Q81887	Q81887 human papil
87	21	22.1	37 1 ME22_EUPRA	P58548 euploetes ra
88	21	22.1	40 1 Y382_TREPA	Q83397 treponema p
89	21	22.1	40 2 Q65775	Q65775 chlamydomon
90	21	22.1	41 2 Q81XX5	Q81xx5 bacillus an
91	21	22.1	41 2 Q8WVY1	Q8wvy1 homo sapien
92	21	22.1	43 2 Q729H4	Q729h4 desulfovibr
93	21	22.1	46 2 Q6D9M9	Q6d9m9 erwinia car
94	21	22.1	46 2 Q70388	Q70388 mesocricetu
95	21	22.1	47 2 Q81883	Q81883 human papil
96	21	22.1	47 2 Q81884	Q81884 human papil
97	21	22.1	49 2 Q7RIA4	Q7ria4 plasmodium
98	21	22.1	50 1 HUNB_PSYCI	Q20332 psychoda ci
99	21	22.1	51 2 Q8CKL0	Q8ckl0 yersinia pe
100	21	22.1	52 2 Q9UHS7	Q9uhs7 homo sapien

ALIGNMENTS

```

[2]
RN  SEQUENCE FROM N.A.
RP  STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA  Strausberg R.;
RL  Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC043705; AAH43705.1; -.
DR  HSSP; P49638; IOIP.
DR  MGD; MGI:1354168; Ttpa.
DR  GO; GO:0005737; C:cytoplasm; TAS.
DR  GO; GO:0008431; P:tocopherol binding; TAS.
DR  GO; GO:0007566; P:embryo implantation; IMP.
DR  GO; GO:0042360; P:vitamin E metabolism; IMP.
DR  InterPro; IPR001251; CRAL_TRIO_C.
DR  Pfam; PF00650; CRAL_TRIO_1.
SQ  SEQUENCE 46 AA, 5488 MW, 926D19CFC2087456 CRC64;

Query Match      26.3%; Score 25; DB 2; Length 46;
Best Local Similarity 60.0%; Pred. No. 5.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy  7 DVCQD 11
    |::|:
Db  22 DICQE 26

RESULT 3
Q716L2
ID  Q716L2 PRELIMINARY; PRT; 50 AA.
AC  Q716L2;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  Gp63.
OS  Mycobacteriophage Pci.
OC  Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX  NCBI_TaxID=213236;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Hatfull G.F., Pedulla M.L., Ford M.E., Houtz J.M., Hendrix R.W.;
RL  Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF547430; AAQ12140.1; -.
SQ  SEQUENCE 50 AA, 5749 MW, 2C4636B7D0D7D526 CRC64;

Query Match      26.3%; Score 25; DB 2; Length 50;
Best Local Similarity 60.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy  7 DVCQD 11
    |::|:
Db  4 EICQD 8

RESULT 4
Q8R194
ID  Q8R194 PRELIMINARY; PRT; 53 AA.
AC  Q8R194;
DT  01-JUN-2002 (TrEMBLrel. 21, Created)
DT  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE  Hypothetical protein (Fragment).
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX  MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Faney J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
RA  Whitting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA  Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA  Jones S.J., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)."
```

```

[2]
RN  SEQUENCE FROM N.A.
RP  STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA  Strausberg R.;
RL  Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC043705; AAH43705.1; -.
DR  HSSP; P49638; IOIP.
DR  MGD; MGI:1354168; Ttpa.
DR  GO; GO:0005737; C:cytoplasm; TAS.
DR  GO; GO:0008431; P:tocopherol binding; TAS.
DR  GO; GO:0007566; P:embryo implantation; IMP.
DR  GO; GO:0042360; P:vitamin E metabolism; IMP.
DR  InterPro; IPR001251; CRAL_TRIO_C.
DR  Pfam; PF00650; CRAL_TRIO_1.
SQ  SEQUENCE 46 AA, 5488 MW, 926D19CFC2087456 CRC64;

Query Match      26.3%; Score 25; DB 2; Length 46;
Best Local Similarity 60.0%; Pred. No. 5.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy  7 DVCQD 11
    |::|:
Db  22 DICQE 26

RESULT 3
Q716L2
ID  Q716L2 PRELIMINARY; PRT; 50 AA.
AC  Q716L2;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  Gp63.
OS  Mycobacteriophage Pci.
OC  Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX  NCBI_TaxID=213236;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Hatfull G.F., Pedulla M.L., Ford M.E., Houtz J.M., Hendrix R.W.;
RL  Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF547430; AAQ12140.1; -.
SQ  SEQUENCE 50 AA, 5749 MW, 2C4636B7D0D7D526 CRC64;

Query Match      26.3%; Score 25; DB 2; Length 50;
Best Local Similarity 60.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy  7 DVCQD 11
    |::|:
Db  4 EICQD 8

RESULT 4
Q8R194
ID  Q8R194 PRELIMINARY; PRT; 53 AA.
AC  Q8R194;
DT  01-JUN-2002 (TrEMBLrel. 21, Created)
DT  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE  Hypothetical protein (Fragment).
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX  MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Faney J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
RA  Whitting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA  Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA  Jones S.J., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)."
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin I.B., Toshiyuki S., Carninci P., Frange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smalilov D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025010; AAB25010.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 53 AA; 5654 MW; 3CF6B0F82CDF02C CRC64;

Query Match 26.3%; Score 25; DB 2; Length 53;
Best Local Similarity 80.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 7 DCCQD 11

RESULT 5
Q87SC2 PRELIMINARY; PRT; 61 AA.
ID Q87SC2
AC Q87SC2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Hypothetical protein VP0502.
GN OrderedLocustNames=VP0502;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
DR EMBL; AP005074; BACS8765.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 61 AA; 7389 MW; 9D179435E86F95C5 CRC64;

Query Match 26.3%; Score 25; DB 2; Length 61;
Best Local Similarity 80.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 49 DVCND 53

RESULT 6
Q8SBL8 PRELIMINARY; PRT; 66 AA.
ID Q8SBL8

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AC Q8SBL8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Gp36 protein.
OS Bacteriophage phi3626.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=190478;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22137838; PubMed=12142405;
RX DOI=10.1128/JB.184.16.4359-4368.2002;
RA Zimmer M., Scherf S., Loessner M.J.;
RT "Genomic analysis of Clostridium perfringens bacteriophage phi3626,
RT which integrates into guaA and possibly affects sporulation.";
RL J. Bacteriol. 184:4359-4368 (2002).
DR EMBL; AY082070; AAL96806.1; -.
SQ SEQUENCE 66 AA; 7937 MW; DC017790FP0158A3 CRC64;

Query Match 26.3%; Score 25; DB 2; Length 66;
Best Local Similarity 60.0%; Pred. No. 7.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCOD 11
Db 18 DICKD 22

RESULT 7
O18888 PRELIMINARY; PRT; 31 AA.
ID O18888
AC O18888;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE Fibrillin 1 (Fragment).
GN Name=FBN1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Ganjam K.K., Shibuya H., Stoy S.J., Ganjam V.K., Katz M.L.,
RA Johnson G.S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029080; AAB84192.1; -.
DR HSSP; P35555; LLMJ.
FT NON_TER 1
FT NON_TER 31
SQ SEQUENCE 31 AA; 3502 MW; 8D13DA183EB44EB5 CRC64;

Query Match 25.3%; Score 24; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 10
Db 17 DVCQD 20

RESULT 8
ME20_EUPRA STANDARD; PRT; 37 AA.
ID ME20_EUPRA
AC P26888;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Mating pheromone Er-20 (Euplome R20) (fragment).
GN Name=MAT20;
OS Euplotes raikovi.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euplotida; Euplotidae; Euplotes.

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OX NCBI_TaxID=5938;
RN [1]
RP SEQUENCE.
RC STRAIN=GA-4;
RA MEDLINE=92196059; PubMed=1549567;
RA Raffioni S., Miceli C., Vallesi A., Chowdhury S.K., Chait B.T.,
RA Luporini P., Bradshaw R.A.;
RT "Primary structure of Euplates raikovi pheromones: comparison of five
RT sequences of pheromones from cells with variable mating
RT interactions.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2071-2075(1992).
CC -!- FUNCTION: Mating ciliate pheromones (or gamones) are diffusible
CC extra-cellular communication signals that distinguish different
CC intraspecific classes of cells commonly referred to as "mating
CC types". They prepare the latter for conjugation by changing their
CC cell surface properties.
CC -!- SUBUNIT: Homodimer (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; C41933; C41933.
DR HSSP; P58548; 1HD6.
DR InterPro; IPR009064; Protoz_pheromone.
DR Pfam; PF06360; E_raikovi_mat; 1.
KW Direct protein sequencing; Pheromone.
FT DISULFID 3 18 By similarity.
FT DISULFID 10 32 By similarity.
FT DISULFID 15 24 By similarity.
FT NON_TER 37 37
FT SEQUENCE 37 AA; 4002 MW; DD8C85FD78F704CF CRC64;

Query Match 25.3%; Score 24; DB 1; Length 37;
Best Local Similarity 60.0%; Pred. No. 7e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 DVCQD 11
|:|:|
Db 1 DICDD 5

RESULT 9
Q6T3W6 PRELIMINARY; PRT; 37 AA.
AC Q6T3W6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Dopa decarboxylase (Fragment).
GN Name=Ddc;
OS Heliconius cydno chioneus.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconius.
OX NCBI_TaxID=171915;
RN [1]
RP SEQUENCE FROM N.A.
RA Bull V., Beltran M., Bermingham E., Jiggins C.D., McMillan W.O. III,
RA Tobler A., Mallet J.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- SIMILARITY: Belongs to the group II decarboxylase family.
DR EMBL; AY437804; AAR04848.1; -.
DR InterPro; IPR002129; Pyridoxal dec.
KW Lyase; Pyridoxal phosphate.
FT NON_TER 1 1
FT NON_TER 37 37
FT SEQUENCE 37 AA; 3838 MW; 2FE8228A77EF94AE CRC64;

Query Match 25.3%; Score 24; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQD 10
|:|:|

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Db 21 DVCQ 24

RESULT 10
Q8DXU1 PRELIMINARY; PRT; 38 AA.
AC Q8DXU1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SAG1755.
GN OrderedLocuNames=SAG1755;
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RC MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
RA Tetelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014271; AAN00618.1; -.
DR TIGR; SAG1755; -.
KW Complete proteome.
SQ SEQUENCE 38 AA; 4377 MW; BBD0BE4155E80EFD CRC64;

Query Match 25.3%; Score 24; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VCQD 11
|:|:|
Db 11 VCQD 14

RESULT 11
Q9DE17 PRELIMINARY; PRT; 38 AA.
AC Q9DE17;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Retinoic acid receptor beta4M' (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20528616; PubMed=11073974;
RX DOI=10.1128/MCB.20.23.8731-8739.2000;
RA Kobayashi M., Yu R.T., Yasuda K., Umesono K.;
RT "Cell-type-specific regulation of the retinoic acid receptor mediated
RT by the orphan nuclear receptor RXR.";
RL Mol. Cell. Biol. 20:8731-8739(2000).
DR EMBL; AF220163; AAG33962.1; -.
DR HSSP; P10826; 1HRA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR008946; Str_ncl_receptor.
KW Receptor.
FT NON_TER 38 38

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SQ SEQUENCE 38 AA; 4205 MW; ED326100D05FE403 CRC64;
Query Match 25.3%; Score 24; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VCQD 11
Db 33 VCQD 36

RESULT 12
Q62V19 PRELIMINARY; PRT; 39 AA.
ID Q62V19;
AC Q62V19;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=BL01620;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
RA Berk A.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus
RT licheniformis and comparisons with closely related Bacillus species.";
RL Genome Biol. 5:R77-R77(2004).
DR EMBL; CP000002; AAU23219.1; -.
KW Hypothetical protein.
SQ SEQUENCE 39 AA; 4463 MW; CEDD838CD4055625 CRC64;

Query Match 25.3%; Score 24; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VCQD 11
Db 5 VCQD 8

RESULT 13
Q9DE18 PRELIMINARY; PRT; 39 AA.
ID Q9DE18;
AC Q9DE18;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Retinoic acid receptor beta4M (fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX DOI=10.1128/MCB.20.23.8731-8739.2000;
RA Kobayashi M., Yu R.T., Yasuda K., Umesono K.;
RT "Cell-type-specific regulation of the retinoic acid receptor mediated
RT by the orphan nuclear receptor TLX.";
RL Mol. Cell. Biol. 20:8731-8739(2000).
DR EMBL; AF220162; AAG33961.1; -.
DR HSP; P10826; 1HRA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR008946; Str_ncl_receptor.

KW Receptor.
FT NON_TER 39
SQ SEQUENCE 39 AA; 4276 MW; 399B6109D667B61F CRC64;
Query Match 25.3%; Score 24; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VCQD 11
Db 34 VCQD 37

RESULT 14
Q732A2 PRELIMINARY; PRT; 42 AA.
ID Q732A2;
AC Q732A2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BCE4013;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.W., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017277; AAS42915.1; -.
DR TIGR; BCE4013; -.
KW Complete proteome.
SQ SEQUENCE 42 AA; 4546 MW; 1FA3D3DF18288B58 CRC64;

Query Match 25.3%; Score 24; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VCQD 11
Db 5 VCQD 8

RESULT 15
Q819L0 PRELIMINARY; PRT; 42 AA.
ID Q819L0;
AC Q819L0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BC3966;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Overbeek R., Pusch G., Haseikorn R., Fonstein M., Ehrlich S.D.,
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017011; AAP10886.1; -.
KW Complete proteome; Hypothetical protein.
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SQ SEQUENCE 42 AA; 4546 MW; 1FA3D3DF18288E58 CRC64;
Query Match 25.3%; Score 24; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VQCD 11
Db 5 VQCD 8

RESULT 16
Q81MR8 PRELIMINARY; PRT; 42 AA.
AC Q81MR8; Q6KN5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BA4176, GBAA4176;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017037; AAP27900.1; -.
DR EMBL; AE017334; AAT33298.1; -.
DR TIGR; BA4176; -.
DR TIGR; GBAA4176; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 42 AA; 4546 MW; 1FA3D3DF18288E58 CRC64;
Query Match 25.3%; Score 24; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VQCD 11
Db 5 VQCD 8

RESULT 17
Q9P0Z7 PRELIMINARY; PRT; 46 AA.
AC Q9P0Z7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Latent transforming growth factor beta binding protein 3

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DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Saharinen J., Penttinen C., Keski-Oja J.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF135961; AAF62353.2; -.
DR HSSP; P35555; ILMJ.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR00152; ASx hydroxyl S.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF07645; EGF_CA; 1.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS0010; ASX HYDROXYL; 1.
DR PROSITE; PS0186; EGF_2; UNKNOWN_1.
DR PROSITE; PS50026; EGF_3; 1.
KW EGF-like domain.
FT NON_TER 1
FT NON_TER 46
SQ SEQUENCE 46 AA; 4971 MW; 211C501D8B844A8C CRC64;
Query Match 25.3%; Score 24; DB 2; Length 46;
Best Local Similarity 80.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 DVCQD 11
Db 2 DECQD 6

RESULT 18
R332 MYCGE STANDARD; PRT; 48 AA.
ID R332 MYCGE STANDARD; PRT; 48 AA.
AC Q92B82;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L33 type 2.
GN Name=tpmG2; OrderedLocustNames=MG055.1;
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G.G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bitt K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
RN [2]
RP IDENTIFICATION.
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bitt K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ribosomal protein L33P family.
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DR EMBL; U93684; AAC71272.1; -;
 DR TIGR; MG055.1; -;
 DR HANAP; MF_00294; -; 1.
 DR InterPro; IPR001705; Ribosomal_L33.
 DR ProDom; PD002595; Ribosomal_L33; 1.
 DR TIGRFAMs; TIGR01023; rpmG_bact; 1.
 DR PROSITE; PS00582; RIBOSOMAL_L33; FALSE_NEG.
 KW Complete proteome; Ribosomal protein.
 SQ SEQUENCE 48 AA; 5946 MW; 33C7A47A3B98B65F CRC64;

Query Match 25.3%; Score 24; DB 1; Length 48;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VQCD 11
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 Db 8 VQCD 11

RESULT 19

R332 MYCPN STANDARD; PRT; 48 AA.
 AC P56850;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 50S ribosomal protein L33 type 2.
 GN Name=rpmG2; OrderedLocusNames=MPN069; ORFNames=MP085.1;
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RA MEDLINE=97105885; PubMed=8948633; DOI=10.1093/nar/24.22.4420;
 RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
 RA Herrmann R.;
 RA "Complete sequence analysis of the genome of the bacterium Mycoplasma
 pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC -!- SIMILARITY: Belongs to the ribosomal protein L33P family.

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DR EMBL; AE000010; AAG34736.1; -;
 DR HANAP; MF_00294; -; 1.
 DR InterPro; IPR001705; Ribosomal_L33.
 DR ProDom; PD002595; Ribosomal_L33; 1.
 DR TIGRFAMs; TIGR01023; rpmG_bact; 1.
 DR PROSITE; PS00582; RIBOSOMAL_L33; FALSE_NEG.
 KW Complete proteome; Ribosomal protein.
 SQ SEQUENCE 48 AA; 5863 MW; 93A1A3157098ABED CRC64;

Query Match 25.3%; Score 24; DB 1; Length 48;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VQCD 11
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 Db 8 VQCD 11

RESULT 20

Q65RU4 PRELIMINARY; PRT; 52 AA.
 AC Q65RJ4;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=MS1809;
 OS Mannheimia succiniciproducens MBEL55E.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Mannheimia.
 OX NCBI_TaxID=221988;
 RN [1]

SEQUENCE FROM N.A.

RP STRAIN=MBEL55E;
 RC Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
 RA Kim C.H., Jeong H., Hur C.-G., Kim J.G.;
 RA "The genome sequence of the capnophilic rumen bacterium Mannheimia
 succiniciproducens.";
 RT succiniciproducens.";
 RL Nat. Biotechnol. 0:0-0(2004).
 DR EMBL; AE016827; AAU38416.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 52 AA; 6304 MW; 4226E560A266FC2D CRC64;

Query Match 25.3%; Score 24; DB 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VQCD 11
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 Db 48 VQCD 51

RESULT 21

Q8RYU2 PRELIMINARY; PRT; 53 AA.
 AC Q8RYU2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE B1156H12.4 protein.
 GN Name=B1156H12.4;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]

Query Match 25.3%; Score 24; DB 2; Length 53;
 Best Local Similarity 60.0%; Pred. No. 1e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 DVCQD 11
|:|
Db 43 DICDD 47

RESULT 22

Q9U7K6 PRELIMINARY; PRT; 54 AA.
AC Q9U7K6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Erythrocyte membrane protein 1 SD102G (Fragment).
GN Name=var;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99404835; PubMed=10477185; DOI=10.1016/S0166-6851(99)00106-1;
RA Ward C.P., Clotey G.T., Dorris M., Ji D.D., Arnot D.E.;
RT "Analysis of Plasmodium falciparum PEMP-1/var genes suggests that
recombination rearranges constrained sequences.";
RL Mol. Biochem. Parasitol. 102:167-177(1999).
DR EMBL; AF127281; AAD52761.1; --.
FT NON_TER 1 1
FT NON_TER 54 54
SQ SEQUENCE 54 AA; 5986 MW; 43552A60661F4D71 CRC64;

Query Match 25.3%; Score 24; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQ 10
|:|
Db 20 DVCQ 23

RESULT 23

Q6L9F5 PRELIMINARY; PRT; 54 AA.
AC Q6L9F5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ferredoxin2.
GN Name=fdx2;
OS Helicobacillus mobilis.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Helicobacteriaceae;
OC Helicobacillus.
OX NCBI_TaxID=28064;
RN [1]
RP SEQUENCE FROM N.A.
RA Hatanaka A., Seo D., Kitashima M., Sakurai H., Inoue K.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB106556; BAD22819.1; --.
DR HSP; Q45560; IBD6.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; Fer4_2
DR PRINTS; PR00353; 4FE4SFRDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW 4Fe-4S; Iron; Iron-sulfur; Metal-binding.
SQ SEQUENCE 54 AA; 5575 MW; 802C376B018E57F7 CRC64;

Query Match 25.3%; Score 24; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQ 10
|:|
Db 13 DVCQ 16

RESULT 25

Q9BMS4 PRELIMINARY; PRT; 55 AA.
AC Q9BMS4;

Qy 8 VCQD 11
|:|
Db 42 VCQD 45

RESULT 24

Q9PDP0 PRELIMINARY; PRT; 54 AA.
AC Q9PDP0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Xf1339;
OS Xylella fastidiosa
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=9a5C;
MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camaigo A.A., Camargo L.E.A., Carraro D.M., Carver H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuranae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.B.N., Martins E.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.B.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.S.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA de Silveira J.P., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Teai S.M., Tsuchiko M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003966; AAP84148.1; --.
DR PIR; H82693; H82693.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR PRINTS; PR00353; 4FE4SFRDOXIN.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 54 AA; 6048 MW; 806E2C5C6659AB1E CRC64;

Query Match 25.3%; Score 24; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQ 10
|:|
Db 13 DVCQ 16

DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Erythrocyte membrane protein 1 (Fragment).
GN Name=varK;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_taxid=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21273141; PubMed=11378202; DOI=10.1016/S0166-6851(01)00266-3;
RA Noviyanti R., Brown G.V., Wickham M.E., Duffy M.F., Cowman A.F.,
RA Reeder J.C.;
RT "Multiple var gene transcripts are expressed in Plasmodium falciparum
RT infected erythrocytes selected for adhesion."
RL Mol. Biochem. Parasitol. 114:227-237(2001).
DR EMBL; AF306405; AAK00866.1; -.
FT NON_TER 1
FT NON_TER 55
SQ SEQUENCE 55 AA; 6150 MW; 95879448374331A3 CRC64;

Query Match 25.3%; Score 24; DB 2; Length 55;
Best Local Similarity 100.0%; Pred.No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DVCQ 10
Db 22 DVCQ 25

Search completed: June 30, 2005, 11:58:42
Job time : 193.123 secs

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OM protein - protein search, using sw model

Run on: June 30, 2005, 11:35:52 ; Search time 162 Seconds
(without alignments)
1247.881 Million cell updates/sec

Title: US-09-743-684A-1

Perfect score: 2789

Sequence: 1 MYALFLLASLLGAAALGPVL.....NTETAAQCNAVEHCKRHWN 524

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1722976 seqs, 385795295 residues

Total number of hits satisfying chosen parameters: 1722976

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2789	100.0	524	16	US-10-408-765A-1207
5	2789	100.0	524	16	US-10-746-442-23
6	2789	100.0	524	16	US-10-428-817A-56
7	2789	100.0	524	16	US-10-801-517-1
8	2789	100.0	524	16	US-10-473-127-1865
9	2789	100.0	524	16	US-10-473-127-1866
10	2789	100.0	524	16	US-10-473-127-1868
11	2789	100.0	524	16	US-10-473-127-1869
12	2789	100.0	524	16	US-09-870-759-61
13	2789	100.0	524	16	US-10-473-127-1871
14	2789	100.0	524	16	US-10-473-127-1873
15	2789	100.0	524	16	US-10-473-127-1879
16	2789	100.0	524	16	US-10-473-127-1880
17	2789	100.0	524	16	US-10-473-127-1881
18	2789	100.0	524	16	US-10-473-127-1882
19	2789	100.0	524	16	US-10-473-127-2041
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21	2777.5	99.6	527	9	US-09-870-759-61
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23	2777.5	99.6	527	14	US-10-060-036-73
24	2777.5	99.6	527	16	US-10-428-817A-57
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29	2767.5	99.2	527	16	US-10-473-127-1872
30	2757.5	98.9	523	9	US-09-767-007A-2
31	2731	97.9	522	16	US-10-618-281-38
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34	1969	70.6	554	14	US-10-205-194-176
35	1201	43.1	521	15	US-10-276-162-1
36	1201	43.1	521	19	US-11-002-844-1
37	1151.5	41.3	227	15	US-10-452-858C-11
38	1139.5	40.9	531	11	US-09-833-245-903
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42	552	19.8	953	15	US-10-267-502-385
43	545	19.5	241	15	US-10-108-260A-4529
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45	539.5	19.3	156	14	US-10-102-806-644
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47	412	14.8	80	9	US-09-753-126-3
48	412	14.8	80	15	US-10-330-697-3
49	412	14.8	80	16	US-10-746-442-24
50	412	14.8	80	16	US-10-801-517-2
51	412	14.8	592	9	US-09-753-126-4
52	412	14.8	592	15	US-10-330-697-4
53	350.5	12.6	381	17	US-10-971-461-27
54	349.5	12.5	381	15	US-10-236-031B-10
55	349.5	12.5	381	15	US-10-295-027-1223
56	292.5	10.5	370	18	US-10-820-155-72
57	267	9.6	50	17	US-10-690-276-721
58	256	9.2	50	17	US-10-690-276-720
59	253	9.1	92	16	US-10-425-115-255417
60	235.5	8.4	216	15	US-10-424-599-276328
61	211	7.6	40	10	US-09-780-438A-1
62	211	7.6	212	15	US-10-424-599-157904
63	204.5	7.3	235	16	US-10-425-115-208623
64	204.5	7.3	246	15	US-10-425-114-41077
65	201	7.2	38	10	US-09-780-438A-2
66	201	7.2	212	15	US-10-424-599-157906
67	200.5	7.2	247	16	US-10-767-701-46076
68	197.5	7.1	239	16	US-10-425-115-208619
69	197	7.1	241	16	US-10-425-115-208621
70	197	7.1	241	16	US-10-425-115-208631
71	197	7.1	252	15	US-10-425-114-55606
72	193.5	6.9	227	16	US-10-767-701-45278
73	186.5	6.7	224	16	US-10-425-115-323614
74	186	6.7	33	16	US-10-425-115-202769
75	184	6.6	243	15	US-10-425-114-67929
76	183.5	6.6	273	16	US-10-425-115-208627
77	181	6.5	237	16	US-10-739-930-8849
78	178.5	6.4	226	16	US-10-437-963-202266
79	175.5	6.3	265	15	US-10-425-114-51535
80	174.5	6.3	232	16	US-10-739-930-7788
81	173.5	6.2	331	16	US-10-425-115-279547
82	169.5	6.1	236	15	US-10-424-599-227975
83	168.5	6.0	181	8	US-08-488-123-12
84	165.5	5.9	241	16	US-10-739-930-10638

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Sequence 24, Appl
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Sequence 4, Appl
Sequence 27, Appl
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Sequence 1223, Ap
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Sequence 721, App
Sequence 720, App
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Sequence 279547,
Sequence 227975,
Sequence 12, Appl
Sequence 10638, A

85 165.5 5.9 246 15 US-10-425-114-60351 Sequence 60351, A
 86 163.5 5.9 226 16 US-10-425-115-279544 Sequence 279544, A
 87 163 5.8 240 16 US-10-425-115-279546 Sequence 279546, A
 88 163 5.8 514 14 US-10-339-351-3 Sequence 3, Appl1
 89 163 5.8 514 17 US-10-937-394-3 Sequence 3, Appl1
 90 162 5.8 514 14 US-10-339-351-1 Sequence 1, Appl1
 91 162 5.8 514 17 US-10-937-394-1 Sequence 1, Appl1
 92 159.5 5.7 281 15 US-10-424-599-205602 Sequence 205602, A
 93 157.5 5.6 282 15 US-10-424-599-205603 Sequence 205603, A
 94 156.5 5.6 507 15 US-10-424-599-245585 Sequence 245585, A
 95 154.5 5.5 176 16 US-10-767-701-55427 Sequence 55427, A
 96 152 5.5 496 16 US-10-437-963-184202 Sequence 184202, A
 97 152 5.4 471 15 US-10-425-114-71427 Sequence 71427, A
 98 152 5.4 503 16 US-10-425-115-340687 Sequence 340687, A
 99 151 5.4 222 16 US-10-425-115-218345 Sequence 218345, A
 100 151 5.4 393 15 US-10-425-114-65142 Sequence 65142, A

ALIGNMENTS

RESULT 1
 US-09-870-759-60
 ; Sequence 60, Application US/09870759
 ; Patent No. US20020177551A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 870759
 ; CURRENT APPLICATION NUMBER: US/09/870,759
 ; CURRENT FILING DATE: 2002-01-14
 ; PRIOR APPLICATION NUMBER: US 60/208,128
 ; PRIOR FILING DATE: 2000-05-30
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 60
 ; LENGTH: 524
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-870-759-60

Query Match 100.0%; Score 2789; DB 9; Length 524;
 Best Local Similarity 100.0%; Pred. No. 1.5e-224;
 Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLLASLLGAALAGPVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
 DB 1 MYALFLLASLLGAALAGPVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60

QY 61 LPCDICKDVTAAAGDMLKDNATEEEILVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
 DB 61 LPCDICKDVTAAAGDMLKDNATEEEILVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120

QY 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVPFMANIPLLLY 180
 DB 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVPFMANIPLLLY 180

QY 181 PDGPRSKPQPKDNGDVQDCIQMVTDIQTAVRTNSTFVQALVHVKEECDRLGGMADI 240
 DB 181 PDGPRSKPQPKDNGDVQDCIQMVTDIQTAVRTNSTFVQALVHVKEECDRLGGMADI 240

QY 241 CKNYISOYSEIAIQMMHMQPKEICALVGFCDVEKEMPOTLVPKAVSKNVI PALELVE 300
 DB 241 CKNYISOYSEIAIQMMHMQPKEICALVGFCDVEKEMPOTLVPKAVSKNVI PALELVE 300

QY 301 PIKKEHVPKSDVYCEVCFVLVKEVTKLIDNNKTEKEILDAFDKMCCKLPSLSSECOEV 360
 DB 301 PIKKEHVPKSDVYCEVCFVLVKEVTKLIDNNKTEKEILDAFDKMCCKLPSLSSECOEV 360

QY 361 VDTYGSSTLSILLBEVSPELVCSMLHLCSTGLPALTVHVTQPKDGGFCEVCKKLGVGLD 420
 DB 361 VDTYGSSTLSILLBEVSPELVCSMLHLCSTGLPALTVHVTQPKDGGFCEVCKKLGVGLD 420

QY 421 RNLEKNSTKQEILAALEKGCSTFLPDPYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480
 DB 421 RNLEKNSTKQEILAALEKGCSTFLPDPYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480

QY 481 ACPSAHKPLLTGTEKCIWGPSYWCQNTETAACNAVEHCCKRHVN 524
 DB 481 ACPSAHKPLLTGTEKCIWGPSYWCQNTETAACNAVEHCCKRHVN 524

RESULT 2
 US-09-751-708A-60
 ; Sequence 60, Application US/09751708A
 ; Publication No. US20030157113A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 751708
 ; CURRENT APPLICATION NUMBER: US/09/751,708A
 ; CURRENT FILING DATE: 2002-10-15
 ; PRIOR APPLICATION NUMBER: US 60/173,371
 ; PRIOR FILING DATE: 1999-12-28
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 60
 ; LENGTH: 524
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-751-708A-60

Query Match 100.0%; Score 2789; DB 10; Length 524;
 Best Local Similarity 100.0%; Pred. No. 1.5e-224;
 Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLLASLLGAALAGPVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
 DB 1 MYALFLLASLLGAALAGPVGLGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60

QY 61 LPCDICKDVTAAAGDMLKDNATEEEILVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
 DB 61 LPCDICKDVTAAAGDMLKDNATEEEILVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120

QY 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVPFMANIPLLLY 180
 DB 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVPFMANIPLLLY 180

QY 181 PDGPRSKPQPKDNGDVQDCIQMVTDIQTAVRTNSTFVQALVHVKEECDRLGGMADI 240
 DB 181 PDGPRSKPQPKDNGDVQDCIQMVTDIQTAVRTNSTFVQALVHVKEECDRLGGMADI 240

QY 241 CKNYISOYSEIAIQMMHMQPKEICALVGFCDVEKEMPOTLVPKAVSKNVI PALELVE 300
 DB 241 CKNYISOYSEIAIQMMHMQPKEICALVGFCDVEKEMPOTLVPKAVSKNVI PALELVE 300

QY 301 PIKKEHVPKSDVYCEVCFVLVKEVTKLIDNNKTEKEILDAFDKMCCKLPSLSSECOEV 360
 DB 301 PIKKEHVPKSDVYCEVCFVLVKEVTKLIDNNKTEKEILDAFDKMCCKLPSLSSECOEV 360

QY 361 VDTYGSSTLSILLBEVSPELVCSMLHLCSTGLPALTVHVTQPKDGGFCEVCKKLGVGLD 420
 DB 361 VDTYGSSTLSILLBEVSPELVCSMLHLCSTGLPALTVHVTQPKDGGFCEVCKKLGVGLD 420

QY 421 RNLEKNSTKQEILAALEKGCSTFLPDPYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480
 DB 421 RNLEKNSTKQEILAALEKGCSTFLPDPYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480

QY 481 ACPSAHKPLLTGTEKCIWGPSYWCQNTETAACNAVEHCCKRHVN 524
 DB 481 ACPSAHKPLLTGTEKCIWGPSYWCQNTETAACNAVEHCCKRHVN 524

RESULT 3
 US-10-267-502-386
 ; Sequence 386, Application US/10267502


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; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 386
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-502-386

Query Match      100.0%; Score 2789; DB 15; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.5e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60
DB 1 MYALFLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKDNATEEELVYLEKTCMDLKPNNMSASCKEIVDSYLVPIIDI 120
DB 61 LPCDICKDVVTAAGDMLKDNATEEELVYLEKTCMDLKPNNMSASCKEIVDSYLVPIIDI 120
QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
DB 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
QY 181 PQDGRSPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
DB 181 PQDGRSPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
QY 241 CKNYISOYSETAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKASKNVIPALELVE 300
DB 241 CKNYISOYSETAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKASKNVIPALELVE 300
QY 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSSECEQEV 360
DB 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSSECEQEV 360
QY 361 VDTYSSILSLILEEVSPELVCSMLHLCSTGTRLPALTTHVTQPKDGGCFCEVCKLGVYLD 420
DB 361 VDTYSSILSLILEEVSPELVCSMLHLCSTGTRLPALTTHVTQPKDGGCFCEVCKLGVYLD 420
QY 421 RNLEKNSTKQETLAALAEKGCFLPDPYQKQCDQFVAEYEPVLIETLVEVMDPSFVCLKIG 480
DB 421 RNLEKNSTKQETLAALAEKGCFLPDPYQKQCDQFVAEYEPVLIETLVEVMDPSFVCLKIG 480
QY 481 ACPSAHKPLLTGTEKINGPSYWCQNTETAAQCNAVEHCKRHVWN 524
DB 481 ACPSAHKPLLTGTEKINGPSYWCQNTETAAQCNAVEHCKRHVWN 524

RESULT 4
US-10-408-765A-1207
; Sequence 1207, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A

; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 386
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-502-386

Query Match      100.0%; Score 2789; DB 15; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.5e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60
DB 1 MYALFLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKDNATEEELVYLEKTCMDLKPNNMSASCKEIVDSYLVPIIDI 120
DB 61 LPCDICKDVVTAAGDMLKDNATEEELVYLEKTCMDLKPNNMSASCKEIVDSYLVPIIDI 120
QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
DB 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
QY 181 PQDGRSPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
DB 181 PQDGRSPQPKDNGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
QY 241 CKNYISOYSETAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKASKNVIPALELVE 300
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QY 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSSECEQEV 360
DB 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPSLSSECEQEV 360
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DB 361 VDTYSSILSLILEEVSPELVCSMLHLCSTGTRLPALTTHVTQPKDGGCFCEVCKLGVYLD 420
QY 421 RNLEKNSTKQETLAALAEKGCFLPDPYQKQCDQFVAEYEPVLIETLVEVMDPSFVCLKIG 480
DB 421 RNLEKNSTKQETLAALAEKGCFLPDPYQKQCDQFVAEYEPVLIETLVEVMDPSFVCLKIG 480
QY 481 ACPSAHKPLLTGTEKINGPSYWCQNTETAAQCNAVEHCKRHVWN 524
DB 481 ACPSAHKPLLTGTEKINGPSYWCQNTETAAQCNAVEHCKRHVWN 524

RESULT 5
US-10-746-442-23
; Sequence 23, Application US/10746442
; Publication No. US20040121958A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN
; FILE REFERENCE: 07256/024001
; CURRENT APPLICATION NUMBER: US/10/746,442
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US/08/928,074
; PRIOR FILING DATE: FILING DATE: 1997-09-11
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 08/611,307
; PRIOR FILING DATE: FILING DATE: 1996-03-05
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: PCT/US97/04143
; PRIOR FILING DATE: FILING DATE: 1996-03-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-746-442-23
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Query Match 100.0%; Score 2789; DB 16; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.5e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60
Db 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60

Qy 61 LPCDICKDVVTAAGDMLKDNATEBEILVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKDVVTAAGDMLKDNATEBEILVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120

Qy 121 IKGMSRPGVCSALNLCESLQKHLAEIHNHOKLESNKI PELDMTEVVAPFMANIPLLLY 180
Db 121 IKGMSRPGVCSALNLCESLQKHLAEIHNHOKLESNKI PELDMTEVVAPFMANIPLLLY 180

Qy 181 PQDGPRSKPQKNDGVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGFGMADI 240
Db 181 PQDGPRSKPQKNDGVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGFGMADI 240

Qy 241 CKNYISOYSEIATQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVI PALELVE 300
Db 241 CKNYISOYSEIATQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVI PALELVE 300

Qy 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCSKL PKSLSEECOE 360
Db 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCSKL PKSLSEECOE 360

Qy 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGTRLPALT VHVTQPKDGGFCVCKKLVG YLD 420
Db 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGTRLPALT VHVTQPKDGGFCVCKKLVG YLD 420

Qy 421 RNLEKNSTKQEBILAALEKGSFLPDYQKQCDQFVAEYEPVLIETLVEWMDPSFVCLKIG 480
Db 421 RNLEKNSTKQEBILAALEKGSFLPDYQKQCDQFVAEYEPVLIETLVEWMDPSFVCLKIG 480

Qy 481 ACPSAHKPLLGTCKIWIWGPSYWCQNTETAACNAVEHCKRHWN 524
Db 481 ACPSAHKPLLGTCKIWIWGPSYWCQNTETAACNAVEHCKRHWN 524

RESULT 6
US-10-428-817A-56
; Sequence 56, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-428-817A-56

Query Match 100.0%; Score 2789; DB 16; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.5e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60
Db 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60

Qy 61 LPCDICKDVVTAAGDMLKDNATEBEILVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKDVVTAAGDMLKDNATEBEILVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120

Qy 121 IKGMSRPGVCSALNLCESLQKHLAEIHNHOKLESNKI PELDMTEVVAPFMANIPLLLY 180
Db 121 IKGMSRPGVCSALNLCESLQKHLAEIHNHOKLESNKI PELDMTEVVAPFMANIPLLLY 180

Qy 181 PQDGPRSKPQKNDGVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGFGMADI 240
Db 181 PQDGPRSKPQKNDGVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGFGMADI 240

Qy 241 CKNYISOYSEIATQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVI PALELVE 300
Db 241 CKNYISOYSEIATQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVI PALELVE 300

Qy 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCSKL PKSLSEECOE 360
Db 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCSKL PKSLSEECOE 360

Qy 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGTRLPALT VHVTQPKDGGFCVCKKLVG YLD 420
Db 361 VDTYSSILSILLEEVSPELVCSMLHLCSTGTRLPALT VHVTQPKDGGFCVCKKLVG YLD 420

Qy 421 RNLEKNSTKQEBILAALEKGSFLPDYQKQCDQFVAEYEPVLIETLVEWMDPSFVCLKIG 480
Db 421 RNLEKNSTKQEBILAALEKGSFLPDYQKQCDQFVAEYEPVLIETLVEWMDPSFVCLKIG 480

Qy 481 ACPSAHKPLLGTCKIWIWGPSYWCQNTETAACNAVEHCKRHWN 524
Db 481 ACPSAHKPLLGTCKIWIWGPSYWCQNTETAACNAVEHCKRHWN 524

RESULT 7
US-10-801-517-1
; Sequence 1, Application US/10801517
; Publication No. US20040229799A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Xiaoyang
; TITLE OF INVENTION: Saposin C-DOPS A Novel Anti-Tumor Agent
; FILE REFERENCE: CHM08/GN003
; CURRENT APPLICATION NUMBER: US/10/801,517
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: 60/465,166
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-801-517-1

Query Match 100.0%; Score 2789; DB 16; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.5e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60
Db 1 MYALFLLASLLGAALAGPVLGLKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60

Qy 61 LPCDICKDVVTAAGDMLKDNATEBEILVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKDVVTAAGDMLKDNATEBEILVLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120

Db 61 LPCDICKDVVTAAGDMLKDNATEEBILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
Db 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
QY 181 PODGPRSPQPKDNGDVCDQCIQWYTDIQTAVRTNSTFVQALVEHVKEBECDBLPGMADI 240
Db 181 PODGPRSPQPKDNGDVCDQCIQWYTDIQTAVRTNSTFVQALVEHVKEBECDBLPGMADI 240
QY 241 CKNYISOYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
Db 241 CKNYISOYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
QY 301 PIKKEHVPAKSDVYCEVCEFLVKEVTYKLIIDNNKTEKILDAFDKMCCKLPKSLSECOEV 360
Db 301 PIKKEHVPAKSDVYCEVCEFLVKEVTYKLIIDNNKTEKILDAFDKMCCKLPKSLSECOEV 360
QY 361 VDTYSSILSILLESVSPELVCSMLHLCSGTGLPALTVHVTQPKDGGFCEVCKKLVGYLD 420
Db 361 VDTYSSILSILLESVSPELVCSMLHLCSGTGLPALTVHVTQPKDGGFCEVCKKLVGYLD 420
QY 421 RNLEKNSTKQETILAALEKGCFLPDYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTKQETILAALEKGCFLPDYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
QY 481 ACPSAHKPLLGTEKICWGPSYWCNTETAACNAVEHCKRHVWN 524
Db 481 ACPSAHKPLLGTEKICWGPSYWCNTETAACNAVEHCKRHVWN 524

RESULT 8

US-10-473-127-1865
; Sequence 1865, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:

; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1865
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1865

Query Match 100.0%; Score 2789; DB 16; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.5e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAFLLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNPPTVKS 60
Db 1 MYAFLLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNPPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKDNATEEBILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKDVVTAAGDMLKDNATEEBILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120

QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
Db 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
QY 181 PODGPRSPQPKDNGDVCDQCIQWYTDIQTAVRTNSTFVQALVEHVKEBECDBLPGMADI 240
Db 181 PODGPRSPQPKDNGDVCDQCIQWYTDIQTAVRTNSTFVQALVEHVKEBECDBLPGMADI 240
QY 241 CKNYISOYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
Db 241 CKNYISOYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
QY 301 PIKKEHVPAKSDVYCEVCEFLVKEVTYKLIIDNNKTEKILDAFDKMCCKLPKSLSECOEV 360
Db 301 PIKKEHVPAKSDVYCEVCEFLVKEVTYKLIIDNNKTEKILDAFDKMCCKLPKSLSECOEV 360
QY 361 VDTYSSILSILLESVSPELVCSMLHLCSGTGLPALTVHVTQPKDGGFCEVCKKLVGYLD 420
Db 361 VDTYSSILSILLESVSPELVCSMLHLCSGTGLPALTVHVTQPKDGGFCEVCKKLVGYLD 420
QY 421 RNLEKNSTKQETILAALEKGCFLPDYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTKQETILAALEKGCFLPDYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
QY 481 ACPSAHKPLLGTEKICWGPSYWCNTETAACNAVEHCKRHVWN 524
Db 481 ACPSAHKPLLGTEKICWGPSYWCNTETAACNAVEHCKRHVWN 524

RESULT 9

US-10-473-127-1866
; Sequence 1866, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:

; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1866
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1866

Query Match 100.0%; Score 2789; DB 16; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.5e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAFLLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNPPTVKS 60
Db 1 MYAFLLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNPPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKDNATEEBILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKDVVTAAGDMLKDNATEEBILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180

Db 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILY 180
Qy 181 PODGPRSKPQKNGDVCQDCIQMVTDTQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
Db 181 PODGPRSKPQKNGDVCQDCIQMVTDTQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
Qy 241 CKNYISQYSEITAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
Db 241 CKNYISQYSEITAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
Qy 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCKSLPKSLSECOEV 360
Db 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCKSLPKSLSECOEV 360
Qy 361 VDTYSSILSLLEBVSPELVCSMLHLCSTGRLPALTVHVTPQKDGGECEVCKKLGVYLD 420
Db 361 VDTYSSILSLLEBVSPELVCSMLHLCSTGRLPALTVHVTPQKDGGECEVCKKLGVYLD 420
Qy 421 RNLEKNSTKQETILAALEKGCFLPDYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480
Db 421 RNLEKNSTKQETILAALEKGCFLPDYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480
Qy 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAAQCNAVEHCKRHWN 524
Db 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAAQCNAVEHCKRHWN 524

RESULT 10

US-10-473-127-1868
; Sequence 1868, Application US/10473127
; Publication No. US20040236091A1

; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1868
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1868

Query Match 100.0%; Score 2789; DB 16; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.5e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYALFLLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNNKPTVKS 60
Db 1 MYALFLLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNNKPTVKS 60
Qy 61 LPCDICKDVVTAAGDMLKDNATEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKDVVTAAGDMLKDNATEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
Qy 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILY 180
Db 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILY 180

Qy 181 PODGPRSKPQKNGDVCQDCIQMVTDTQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
Db 181 PODGPRSKPQKNGDVCQDCIQMVTDTQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
Qy 241 CKNYISQYSEITAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
Db 241 CKNYISQYSEITAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
Qy 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCKSLPKSLSECOEV 360
Db 301 PIKKEHVPKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKMCKSLPKSLSECOEV 360
Qy 361 VDTYSSILSLLEBVSPELVCSMLHLCSTGRLPALTVHVTPQKDGGECEVCKKLGVYLD 420
Db 361 VDTYSSILSLLEBVSPELVCSMLHLCSTGRLPALTVHVTPQKDGGECEVCKKLGVYLD 420
Qy 421 RNLEKNSTKQETILAALEKGCFLPDYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480
Db 421 RNLEKNSTKQETILAALEKGCFLPDYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480
Qy 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAAQCNAVEHCKRHWN 524
Db 481 ACPSAHKPLLGTEKCIWGPSYWCNTETAAQCNAVEHCKRHWN 524

RESULT 11

US-10-473-127-1869
; Sequence 1869, Application US/10473127
; Publication No. US20040236091A1

; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1869
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1869

Query Match 100.0%; Score 2789; DB 16; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.5e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYALFLLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNNKPTVKS 60
Db 1 MYALFLLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNNKPTVKS 60
Qy 61 LPCDICKDVVTAAGDMLKDNATEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKDVVTAAGDMLKDNATEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
Qy 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILY 180
Db 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILY 180
Qy 181 PODGPRSKPQKNGDVCQDCIQMVTDTQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240

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Db 181 PDGPRSKPQKNDGVDVCDQCIQWTDIQTAVRTNSTFVQALVEHVHKBECBRLGPGMADI 240
Qy 241 CKNYISQYSEIAIQMMHMQPKKEICALVGFCDCEVKEMPMQTLVPAKVASKNVIPAELVE 300
Db 241 CKNYISQYSEIAIQMMHMQPKKEICALVGFCDCEVKEMPMQTLVPAKVASKNVIPAELVE 300
Qy 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKWCCKLPKSLSECEQEV 360
Db 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKWCCKLPKSLSECEQEV 360
Qy 361 VDTYSSILSILLEVSPELVCSMLHLCSTGTRLPALTTHVTQPKDGGFCEVCKKLVGYLD 420
Db 361 VDTYSSILSILLEVSPELVCSMLHLCSTGTRLPALTTHVTQPKDGGFCEVCKKLVGYLD 420
Qy 421 RNLEKNSKTQETILAALEKGCSPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSKTQETILAALEKGCSPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Qy 481 ACPSAHKPLLTGTEKCIWGPSYWCNTETAACNAVEHCKRHVN 524
Db 481 ACPSAHKPLLTGTEKCIWGPSYWCNTETAACNAVEHCKRHVN 524
```

RESULT 12

US-10-473-127-1871

; Sequence 1871, Application US/10473127

; Publication No. US20040236091A1

; GENERAL INFORMATION:

; APPLICANT: Zycos Inc.

; TITLE OF INVENTION: TRANSLATIONAL PROFILING

; FILE REFERENCE: 08191-026W01

; CURRENT APPLICATION NUMBER: US/10/473,127

; CURRENT FILING DATE: 2003-09-26

; PRIOR APPLICATION NUMBER: 60/279,495

; FILING DATE: 2001-03-28

; PRIOR APPLICATION NUMBER: 60/292,544

; PRIOR FILING DATE: 2001-05-21

; PRIOR APPLICATION NUMBER: 60/310,801

; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/326,370

; PRIOR FILING DATE: 2001-10-01

; PRIOR APPLICATION NUMBER: 60/336,780

; PRIOR FILING DATE: 2001-12-04

; PRIOR APPLICATION NUMBER: 60/358,985

; PRIOR FILING DATE: 2002-02-20

; NUMBER OF SEQ ID NOS: 2041

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1871

; LENGTH: 524

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-473-127-1871

```
Query Match 100.0%; Score 2789; DB 16; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.5e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYAFLLASLLGAALAGPVLGLKECTRGSAVMQNVKTASDCGAVKHCLQTVWNPPTVKS 60
Db 1 MYAFLLASLLGAALAGPVLGLKECTRGSAVMQNVKTASDCGAVKHCLQTVWNPPTVKS 60

Qy 61 LPCDICKDVVTAAGDMLKDNATEEBILVYLEKTCDWLPKPNNSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKDVVTAAGDMLKDNATEEBILVYLEKTCDWLPKPNNSASCKEIVDSYLPVILDI 120

Qy 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFMANIPLILY 180
Db 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFMANIPLILY 180

Qy 181 PDGPRSKPQKNDGVDVCDQCIQWTDIQTAVRTNSTFVQALVEHVHKBECBRLGPGMADI 240
Db 181 PDGPRSKPQKNDGVDVCDQCIQWTDIQTAVRTNSTFVQALVEHVHKBECBRLGPGMADI 240
```

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Qy 241 CKNYISQYSEIAIQMMHMQPKKEICALVGFCDCEVKEMPMQTLVPAKVASKNVIPAELVE 300
Db 241 CKNYISQYSEIAIQMMHMQPKKEICALVGFCDCEVKEMPMQTLVPAKVASKNVIPAELVE 300
Qy 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKWCCKLPKSLSECEQEV 360
Db 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKWCCKLPKSLSECEQEV 360
Qy 361 VDTYSSILSILLEVSPELVCSMLHLCSTGTRLPALTTHVTQPKDGGFCEVCKKLVGYLD 420
Db 361 VDTYSSILSILLEVSPELVCSMLHLCSTGTRLPALTTHVTQPKDGGFCEVCKKLVGYLD 420
Qy 421 RNLEKNSKTQETILAALEKGCSPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSKTQETILAALEKGCSPDPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Qy 481 ACPSAHKPLLTGTEKCIWGPSYWCNTETAACNAVEHCKRHVN 524
Db 481 ACPSAHKPLLTGTEKCIWGPSYWCNTETAACNAVEHCKRHVN 524
```

RESULT 13

US-10-473-127-1873

; Sequence 1873, Application US/10473127

; Publication No. US20040236091A1

; GENERAL INFORMATION:

; APPLICANT: Zycos Inc.

; TITLE OF INVENTION: TRANSLATIONAL PROFILING

; FILE REFERENCE: 08191-026W01

; CURRENT APPLICATION NUMBER: US/10/473,127

; CURRENT FILING DATE: 2003-09-26

; PRIOR APPLICATION NUMBER: 60/279,495

; PRIOR FILING DATE: 2001-03-28

; PRIOR APPLICATION NUMBER: 60/292,544

; PRIOR FILING DATE: 2001-05-21

; PRIOR APPLICATION NUMBER: 60/310,801

; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/326,370

; PRIOR FILING DATE: 2001-10-01

; PRIOR APPLICATION NUMBER: 60/336,780

; PRIOR FILING DATE: 2001-12-04

; PRIOR APPLICATION NUMBER: 60/358,985

; PRIOR FILING DATE: 2002-02-20

; NUMBER OF SEQ ID NOS: 2041

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1873

; LENGTH: 524

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-473-127-1873

```
Query Match 100.0%; Score 2789; DB 16; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.5e-224;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYAFLLASLLGAALAGPVLGLKECTRGSAVMQNVKTASDCGAVKHCLQTVWNPPTVKS 60
Db 1 MYAFLLASLLGAALAGPVLGLKECTRGSAVMQNVKTASDCGAVKHCLQTVWNPPTVKS 60

Qy 61 LPCDICKDVVTAAGDMLKDNATEEBILVYLEKTCDWLPKPNNSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKDVVTAAGDMLKDNATEEBILVYLEKTCDWLPKPNNSASCKEIVDSYLPVILDI 120

Qy 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFMANIPLILY 180
Db 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAFFMANIPLILY 180

Qy 181 PDGPRSKPQKNDGVDVCDQCIQWTDIQTAVRTNSTFVQALVEHVHKBECBRLGPGMADI 240
Db 181 PDGPRSKPQKNDGVDVCDQCIQWTDIQTAVRTNSTFVQALVEHVHKBECBRLGPGMADI 240

Qy 241 CKNYISQYSEIAIQMMHMQPKKEICALVGFCDCEVKEMPMQTLVPAKVASKNVIPAELVE 300
Db 241 CKNYISQYSEIAIQMMHMQPKKEICALVGFCDCEVKEMPMQTLVPAKVASKNVIPAELVE 300
```

Db 241 CKNYISOYSEIAIQMMHMQPKEICALVGFCDCEVKEMPQTLVPAKVASKNVIPALELVE 300
 Qy 301 PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCSKLPKSLSECOEV 360
 Db 301 PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCSKLPKSLSECOEV 360
 Qy 361 VDTYSSILSLLEBVSPELVCSMLHLCGSTRLPALTTHVTQPKDGGFCFVCKKLVGYLD 420
 Db 361 VDTYSSILSLLEBVSPELVCSMLHLCGSTRLPALTTHVTQPKDGGFCFVCKKLVGYLD 420
 Qy 421 RNLEKNSTKQIBLAALBKCSFLPDYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480
 Db 421 RNLEKNSTKQIBLAALBKCSFLPDYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480
 Qy 481 ACPSAHKPLLGTEKCIWGPSYWCQNTETAACNAVEHCKRHVN 524
 Db 481 ACPSAHKPLLGTEKCIWGPSYWCQNTETAACNAVEHCKRHVN 524

RESULT 14.
 US-10-473-127-1878
 ; Sequence 1878, Application US/10473127
 ; Publication No. US20040236091A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zycos Inc.
 ; TITLE OF INVENTION: TRANSLATIONAL PROFILING
 ; FILE REFERENCE: 08191-026W01
 ; CURRENT APPLICATION NUMBER: US/10/473,127
 ; CURRENT FILING DATE: 2003-09-26
 ; PRIOR APPLICATION NUMBER: 60/279,495
 ; PRIOR FILING DATE: 2001-03-28
 ; PRIOR APPLICATION NUMBER: 60/292,544
 ; PRIOR FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: 60/310,801
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/326,370
 ; PRIOR FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: 60/336,780
 ; PRIOR FILING DATE: 2001-12-04
 ; PRIOR APPLICATION NUMBER: 60/358,985
 ; PRIOR FILING DATE: 2002-02-20
 ; NUMBER OF SEQ ID NOS: 2041
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1878
 ; LENGTH: 524
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Query Match 100.0%; Score 2789; DB 16; Length 524;
 Best Local Similarity 100.0%; Pred. No. 1.5e-224;
 Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MYALLFLASLLGAALAGPVLGLKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNNKPTVKS 60
 Db 1 MYALLFLASLLGAALAGPVLGLKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNNKPTVKS 60
 Qy 61 LPCDICKDVVTAAGDMLKDNATEEBILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
 Db 61 LPCDICKDVVTAAGDMLKDNATEEBILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
 Qy 121 IKGMSRPGVCSALNLCESLQKHLAEINHQLESNKIPELDMTEVVAPFWMANIPLLLY 180
 Db 121 IKGMSRPGVCSALNLCESLQKHLAEINHQLESNKIPELDMTEVVAPFWMANIPLLLY 180
 Qy 181 PQDGRSKPQKNGDVQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPMADI 240
 Db 181 PQDGRSKPQKNGDVQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPMADI 240
 Qy 241 CKNYISOYSEIAIQMMHMQPKEICALVGFCDCEVKEMPQTLVPAKVASKNVIPALELVE 300
 Db 241 CKNYISOYSEIAIQMMHMQPKEICALVGFCDCEVKEMPQTLVPAKVASKNVIPALELVE 300

Qy 301 PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCSKLPKSLSECOEV 360
 Db 301 PIKKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCSKLPKSLSECOEV 360
 Qy 361 VDTYSSILSLLEBVSPELVCSMLHLCGSTRLPALTTHVTQPKDGGFCFVCKKLVGYLD 420
 Db 361 VDTYSSILSLLEBVSPELVCSMLHLCGSTRLPALTTHVTQPKDGGFCFVCKKLVGYLD 420
 Qy 421 RNLEKNSTKQIBLAALBKCSFLPDYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480
 Db 421 RNLEKNSTKQIBLAALBKCSFLPDYQKQCDQFVAEYEPVLIELVEMDPSFVCLKIG 480
 Qy 481 ACPSAHKPLLGTEKCIWGPSYWCQNTETAACNAVEHCKRHVN 524
 Db 481 ACPSAHKPLLGTEKCIWGPSYWCQNTETAACNAVEHCKRHVN 524

RESULT 15
 US-10-473-127-1879
 ; Sequence 1879, Application US/10473127
 ; Publication No. US20040236091A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zycos Inc.
 ; TITLE OF INVENTION: TRANSLATIONAL PROFILING
 ; FILE REFERENCE: 08191-026W01
 ; CURRENT APPLICATION NUMBER: US/10/473,127
 ; CURRENT FILING DATE: 2003-09-26
 ; PRIOR APPLICATION NUMBER: 60/279,495
 ; PRIOR FILING DATE: 2001-03-28
 ; PRIOR APPLICATION NUMBER: 60/292,544
 ; PRIOR FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: 60/310,801
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/326,370
 ; PRIOR FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: 60/336,780
 ; PRIOR FILING DATE: 2001-12-04
 ; PRIOR APPLICATION NUMBER: 60/358,985
 ; PRIOR FILING DATE: 2002-02-20
 ; NUMBER OF SEQ ID NOS: 2041
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1879
 ; LENGTH: 524
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Query Match 100.0%; Score 2789; DB 16; Length 524;
 Best Local Similarity 100.0%; Pred. No. 1.5e-224;
 Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Qy 121 IKGMSRPGVCSALNLCESLQKHLAEINHQLESNKIPELDMTEVVAPFWMANIPLLLY 180
 Db 121 IKGMSRPGVCSALNLCESLQKHLAEINHQLESNKIPELDMTEVVAPFWMANIPLLLY 180
 Qy 181 PQDGRSKPQKNGDVQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPMADI 240
 Db 181 PQDGRSKPQKNGDVQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPMADI 240
 Qy 241 CKNYISOYSEIAIQMMHMQPKEICALVGFCDCEVKEMPQTLVPAKVASKNVIPALELVE 300
 Db 241 CKNYISOYSEIAIQMMHMQPKEICALVGFCDCEVKEMPQTLVPAKVASKNVIPALELVE 300
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Db	481	ACPSAHKPLLGTCKIWGSPYWCNTETAAQCNAVEHCKRHVWN	524

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Job time : 164 secs

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OM protein - protein search, using sw model

Run on: June 30, 2005, 11:29:46 ; Search time 24 Seconds
(without alignments)
1629.838 Million cell updates/sec

Title: US-09-743-684A-1
Perfect score: 2789
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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2789	100.0	524	4	US-09-352-548-1
2	2789	100.0	524	4	US-09-949-016-6272
3	2789	100.0	535	4	US-09-949-016-8603
4	2766.5	99.2	523	1	US-08-100-247-2
5	2766.5	99.2	523	1	US-08-756-031-2
6	2759.5	98.9	523	1	US-08-232-513A-3
7	2759.5	98.9	523	1	US-08-483-146A-2
8	2757.5	98.9	523	1	US-08-484-594A-2
9	2757.5	98.9	523	4	US-09-076-258A-2
10	431	15.5	81	4	US-09-352-548-2
11	418.5	15.0	80	2	US-08-584-671-15
12	418.5	15.0	80	3	US-09-027-376-15
13	415.5	14.9	80	3	US-09-094-192-15
14	412	14.8	80	1	US-08-100-247-3
15	412	14.8	80	1	US-08-483-146A-3
16	412	14.8	80	1	US-08-232-513A-4
17	412	14.8	80	1	US-08-484-594A-3
18	412	14.8	80	4	US-09-076-258A-3
19	412	14.8	80	4	US-08-756-031-3
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22	327	11.7	61	2	US-08-584-671-13
23	327	11.7	61	3	US-09-027-376-13
24	327	11.7	61	3	US-09-094-192-13
25	327	11.7	69	3	US-09-268-070-2
26	322	11.5	79	2	US-08-584-671-16
27	322	11.5	79	3	US-09-027-376-16

28	322	11.5	79	3	US-09-094-192-16	Sequence 16, Appl
29	321	11.5	79	2	US-08-584-671-14	Sequence 14, Appl
30	321	11.5	79	3	US-09-027-376-14	Sequence 14, Appl
31	321	11.5	79	3	US-09-094-192-14	Sequence 14, Appl
32	268.5	9.6	257	3	US-08-596-684F-7	Sequence 7, Appl
33	239.5	8.6	60	2	US-08-584-671-12	Sequence 12, Appl
34	239.5	8.6	60	3	US-09-027-376-12	Sequence 12, Appl
35	239.5	8.6	60	3	US-09-268-070-4	Sequence 4, Appl
36	239.5	8.6	60	3	US-09-094-192-12	Sequence 12, Appl
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38	208	7.5	67	3	US-09-268-070-3	Sequence 3, Appl
39	168.5	6.0	181	3	US-08-848-580-12	Sequence 12, Appl
40	168.5	6.0	181	4	US-08-488-123-12	Sequence 12, Appl
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42	162	5.8	514	4	US-10-339-351-1	Sequence 1, Appl
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44	141.5	5.1	514	4	US-10-339-351-2	Sequence 2, Appl
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47	126.5	4.5	514	4	US-09-107-532A-6282	Sequence 6282, Ap
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49	118	4.2	894	4	US-09-949-016-10324	Sequence 10324, A
50	115.5	4.1	1002	4	US-09-762-724-4	Sequence 4, Appl
51	114.5	4.1	1001	4	US-09-949-016-9832	Sequence 9832, Ap
52	113	4.1	1027	4	US-09-762-724-8	Sequence 8, Appl
53	113	4.1	1786	3	US-08-973-462-8	Sequence 2, Appl
54	112.5	4.0	1014	4	US-09-762-724-2	Sequence 2, Appl
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59	111	4.0	22	1	US-08-232-513A-20	Sequence 20, Appl
60	111	4.0	22	1	US-08-484-594A-1	Sequence 1, Appl
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64	111	4.0	22	4	US-09-148-030-1	Sequence 1, Appl
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67	111	4.0	22	4	US-08-756-031-1	Sequence 1, Appl
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71	109	3.9	1029	4	US-09-762-724-6	Sequence 6, Appl
72	109	3.9	1341	4	US-09-248-796A-19074	Sequence 19074, A
73	108	3.9	451	4	US-09-107-532A-6444	Sequence 6444, Ap
74	108	3.9	1078	4	US-09-248-796A-20284	Sequence 20284, A
75	107.5	3.9	739	4	US-09-270-767-46376	Sequence 46376, A
76	106	3.8	22	3	US-08-231-159-8	Sequence 8, Appl
77	106	3.8	22	3	US-08-611-307-8	Sequence 8, Appl
78	106	3.8	1009	4	US-09-762-724-10	Sequence 10, Appl
79	105.5	3.8	483	4	US-09-134-000C-3796	Sequence 3796, Ap
80	105.5	3.8	764	4	US-09-370-838-67	Sequence 67, Appl
81	105.5	3.8	764	4	US-09-538-092-944	Sequence 944, App
82	105.5	3.8	764	4	US-08-854-133-67	Sequence 67, Appl
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84	105.5	3.8	979	4	US-09-543-681A-5466	Sequence 5466, Ap
85	105	3.8	458	6	5177002-2	Patent No. 5177002
86	105	3.8	458	6	5177002-2	Patent No. 5177002
87	105	3.8	474	1	US-08-222-619-5	Sequence 5, Appl
88	105	3.8	474	4	US-09-949-016-11630	Sequence 11630, A
89	105	3.8	474	5	PCT-US95-04075-5	Sequence 5, Appl
90	104.5	3.7	517	4	US-09-257-825B-21	Sequence 21, Appl
91	104.5	3.7	630	4	US-09-248-796A-20275	Sequence 20275, A
92	104.5	3.7	1017	4	US-09-762-724-12	Sequence 12, Appl
93	104	3.7	554	4	US-09-248-796A-19033	Sequence 19033, A
94	103.5	3.7	1729	4	US-09-553-630-2	Sequence 2, Appl
95	103	3.7	1038	4	US-09-538-092-487	Sequence 487, App
96	102	3.7	458	6	5177002-1	Patent No. 5177002
97	102	3.7	458	6	5177002-1	Patent No. 5177002
98	102	3.7	458	6	5177002-1	Patent No. 5177002
99	102	3.7	474	4	US-09-949-016-5963	Sequence 5963, Ap
100	102	3.7	569	4	US-09-949-016-11036	Sequence 11036, A

ALIGNMENTS

RESULT 1
US-09-352-548-1
; Sequence 1, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: prosaposin
; NAME/KEY: PEPTIDE
; LOCATION: (195)..(275)
; OTHER INFORMATION: Saposin B
US-09-352-548-1

Query Match 100.0%; Score 2789; DB 4; Length 524;
Best Local Similarity 100.0%; Pred. No. 2e-242;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILLY 180

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Db 181 PQDGRSKPQKNDGVCQDCIQWVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240

Qy 301 PIKXHEVPAKSDVYCEVCEFLVKEVTCLIIDNNKTEKEILDADFDMKCSKLPKSLSEECQEV 360
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Qy 361 VDTYSSILSLILEEVSPELVCSMLHLCSGTRLPALT VHVTQPKDGGFCFVCKKLGVYLD 420
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Qy 481 ACPSAHKPFLTGTEKCIWGPSYWCQNTETAAQNAVEHCKRHVWN 524
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RESULT 2

US-09-949-016-6272
; Sequence 6272, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6272
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6272

Query Match 100.0%; Score 2789; DB 4; Length 524;
Best Local Similarity 100.0%; Pred. No. 2e-242;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 241 CKNYISQYSEITAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVI PALELVE 300

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Db 301 PIKXHEVPAKSDVYCEVCEFLVKEVTCLIIDNNKTEKEILDADFDMKCSKLPKSLSEECQEV 360

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Db 361 VDTYSSILSLILEEVSPELVCSMLHLCSGTRLPALT VHVTQPKDGGFCFVCKKLGVYLD 420

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Db 421 RNLEKNSTKQEILAALEKGCFLPDPYQKQCDQFVAEYEPVLIETILVEVMDPSFVCLKIG 480

Qy 481 ACPSAHKPFLTGTEKCIWGPSYWCQNTETAAQNAVEHCKRHVWN 524
Db 481 ACPSAHKPFLTGTEKCIWGPSYWCQNTETAAQNAVEHCKRHVWN 524

RESULT 3

US-09-949-016-8603
; Sequence 8603, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8603
 ; LENGTH: 535
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-8603

Query Match 100.0%; Score 2789; DB 4; Length 535;
 Best Local Similarity 100.0%; Pred. No. 2.1e-242;
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 DB 12 MYALFLLASLLGAALAGPVLGKCTRGSAVWCQNVKTASDCGAVKHCLQTVWNNKPTVKS 71
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 DB 72 LPCDICKDVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNMSASCKEIVDSYLVILDI 131
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 DB 312 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCVKLPKSLSECEQEV 371
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 DB 492 ACPSAHKPLLGTEKICWGPSYWCQNTETAACNAVEHCKRHWN 535

RESULT 4

US-08-100-247-2
 ; Sequence 2, Application US/08100247
 ; Patent No. 5571787
 ; GENERAL INFORMATION:
 ; APPLICANT: O'BRIEN, JOHN S.
 ; APPLICANT: KISHIMOTO, YASUO
 ; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
 ; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
 ; CITY: NEWPORT BEACH
 ; STATE: CA

; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/100,247
 ; FILING DATE: 19930730
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Israelsen, Ned A.
 ; REGISTRATION NUMBER: 29,655
 ; REFERENCE/DOCKET NUMBER: O'Brien.002A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-235-8550
 ; TELEFAX: 619-235-0176
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 523 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; IMMEDIATE SOURCE:
 ; CLONE: PROSAPOSIN
 ; US-08-100-247-2
 Query Match 99.2%; Score 2766.5; DB 1; Length 523;
 Best Local Similarity 99.4%; Pred. No. 2.1e-240;
 Matches 521; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MYALFLLASLLGAALAGPVLGKCTRGSAVWCQNVKTASDCGAVKHCLQTVWNNKPTVKS 60
 DB 1 MYALFLLASLLGAALAGPVLGKCTRGSAVWCQNVKTASDCGAVKHCLQTVWNNKPTVKS 60
 QY 61 LPCDICKDVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNMSASCKEIVDSYLVILDI 120
 DB 61 LPCDICKDVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNMSASCKEIVDSYLVILDI 120
 QY 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
 DB 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
 QY 181 PDGPRSKPQKNDGVCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPMADI 240
 DB 181 PDGPRSKPQKNDGVCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPMADI 239
 QY 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPAELVE 300
 DB 240 CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPAELVE 299
 QY 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCVKLPKSLSECEQEV 360
 DB 300 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCVKLPKSLSECEQEV 359
 QY 361 VDTYSSILSLLEEVSPPELVCSMLHLCSTGLPALTVHVTQPKDGGFCVCKLVGLYD 420
 DB 360 VDTYSSILSLLEEVSPPELVCSMLHLCSTGLPALTVHVTQPKDGGFCVCKLVGLYD 419
 QY 421 RNLEKNSTKQEILAALEKGCFLPDYQKQCDQFVAEYEPVLIETILVEVMDPSFVCLKIG 480
 DB 420 RNLEKNSTKQEILAALEKGCFLPDYQKQCDQFVAEYEPVLIETILVEVMDPSFVCLKIG 479
 QY 481 ACPSAHKPLLGTEKICWGPSYWCQNTETAACNAVEHCKRHWN 524
 DB 480 ACPSAHKPLLGTEKICWGPSYWCQNTETAACNAVEHCKRHWN 523

RESULT 5
US-08-756-031-2
; Sequence 2, Application US/08756031
; Patent No. 6590074
; GENERAL INFORMATION:
; APPLICANT: O'BRIEN, JOHN S.
; APPLICANT: KISHIMOTO, YASUO
; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
; CITY: NEWPORT BEACH
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,031
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: OBR1EN.002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; IMMEDIATE SOURCE:
; CLONE: PROSAPOSIN

US-08-756-031-2
Query Match 99.2%; Score 2766.5; DB 4; Length 523;
Best Local Similarity 99.4%; Pred. No. 2.1e-240;
Matches 521; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
QY 1 MYAFLLASLLGAALAGPVGLGKCTRGSAVWCNQVKTASDCGAVKHCLQTVWNNKPTVKS 60
Db 1 MYAFLLASLLGAALAGPVGLGKCTRGSAVWCNQVKTASDCGAVKHCLQTVWNNKPTVKS 60
QY 61 LPDCICKDVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPDCICKDVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
QY 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVPFMANIPLLLY 180
Db 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVPFMANIPLLLY 180
QY 181 PDGPRSKPQPKNDGVQDCQIMVTDIQTAVRTNSTFVQALVEHVKECDRLGFGMADI 240
Db 181 PDGPRSKPQPKD-GDVQDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGFGMADI 239
QY 241 CKNYISQVSEIATIQMMHMQPKIEICALVGFCDVEKEMPMTOTLVPAKVASKNVI PALELVE 300
Db 240 CKNYISQVSEIATIQMMHMQPKIEICALVGFCDVEKEMPMTOTLVPAKVASKNVI PALELDLV 299

QY 301 PIKKEHPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLPKSLSEECQEV 360
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300 PIKKEHPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLPKSLSEECQEV 359
QY 361 VDTYSSILSILLBEVSPVCSMLHLCSTGTRLPALTWHVTQPKDGGFCVCKKLGVYLD 420
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
360 VDTYSSILSILLBEVSPVCSMLHLCSTGTRLPALTWHVTQPKDGGFCVCKKLGVYLD 419
QY 421 RNLEKNSTKOBILAALEKGGSFDPYQKOCDDQVAEYEPVLIEILVEVMDPSFVCLKIG 480
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
420 RNLEKNSTKOBILAALEKGGSFDPYQKOCDDQVAEYEPVLIEILVEVMDPSFVCLKIG 479
QY 481 ACPGAHKPLLGTEKCIWGPSYWCQNTETAACNAVEHCKRHVN 524
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
480 ACPGAHKPLLGTEKCIWGPSYWCQNTETAACNAVEHCKRHVN 523

RESULT 6
US-08-232-513A-3
; Sequence 3, Application US/08232513A
; Patent No. 5700909
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides
; TITLE OF INVENTION: as Therapeutic Agents
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,513A
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1643
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..523
; OTHER INFORMATION: /label= Hum_prosaposin
US-08-232-513A-3

Query Match 98.9%; Score 2759.5; DB 1; Length 523;
Best Local Similarity 99.2%; Pred. No. 9.1e-240;
Matches 520; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
QY 1 MYAFLLASLLGAALAGPVGLGKCTRGSAVWCNQVKTASDCGAVKHCLQTVWNNKPTVKS 60
Db 1 MYAFLLASLLGAALAGPVGLGKCTRGSAVWCNQVKTASDCGAVKHCLQTVWNNKPTVKS 60
QY 61 LPDCICKDVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120

Db 61 LPDCICKDVVTAAGDMLKDNATEBEILVYLGKTCDWLPKPNMSASCKEIVDSYLPVILI 120
Qy 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILLY 180
Db 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILLY 180
Qy 181 PDGPRSPQPKD-GDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGGMADI 240
Db 181 PDGPRSPQPKD-GDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGGMADI 239
Qy 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDCEVKEMPMQTLVPAKVASKNVI PALELVE 300
Db 240 CKNYISQYSEIAIQMMHMQPKEICALVGFCDCEVKEMPMQTLVPAKVASKNVI PALDLVD 299
Qy 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMKCSKLPKLSSECEQEV 360
Db 300 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMKCSKLPKLSSECEQEV 359
Qy 361 VDTYSSILSLLEEVSPELVCSMLHLCGSGTRLPALTVHVTPQKDGCFCEVCKKLVGYLD 420
Db 360 VDTYSSILSLLEEVSPELVCSMLHLCGSGTRLPALTVHVTPQKDGCFCEVCKKLVGYLD 419
Qy 421 RNLEKNSTKQETLAALKEGCSFLDPYQKQCDQFVAEYEPVLIETLVEMDPSFVCLKIG 480
Db 420 RNLEKNSTKQETLAALKEGCSFLDPYQKQCDQFVAEYEPVLIETLVEMDPSFVCLKIG 479
Qy 481 ACPSAHKPLLGTETKCIWGPSYWCNTETAACNAVEHCKRHWN 524
Db 480 ACPSAHKPLLGTETKCIWGPSYWCNTETAACNAVEHCKRHWN 523

RESULT 7
US-08-483-146A-2
; Sequence 2, Application US/08483146A
; Patent No. 5696080
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Blvd. 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483.146A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: MELOS.002DV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-483-146A-2
Query Match 98.9%; Score 2757.5; DB 1; Length 523;
Best Local Similarity 99.2%; Pred. No. 1.4e-239;
Matches 520; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
Qy 1 MYALFLASLGLAALAGPVLGLKECTRGSAVWCVNKTASDCGAVKHCLQTVNNKPTVKS 60
Db 1 MYALFLASLGLAALAGPVLGLKECTRGSAVWCVNKTASDCGAVKHCLQTVNNKPTVKS 60
Qy 61 LPDCICKDVVTAAGDMLKDNATEBEILVYLGKTCDWLPKPNMSASCKEIVDSYLPVILI 120
Db 61 LPDCICKDVVTAAGDMLKDNATEBEILVYLGKTCDWLPKPNMSASCKEIVDSYLPVILI 120
Qy 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILLY 180
Db 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILLY 180
Qy 181 PDGPRSPQPKD-GDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGGMADI 240
Db 181 PDGPRSPQPKD-GDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGGMADI 239
Qy 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDCEVKEMPMQTLVPAKVASKNVI PALELVE 300
Db 240 CKNYISQYSEIAIQMMHMQPKEICALVGFCDCEVKEMPMQTLVPAKVASKNVI PALDLVD 299
Qy 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMKCSKLPKLSSECEQEV 360
Db 300 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMKCSKLPKLSSECEQEV 359
Qy 361 VDTYSSILSLLEEVSPELVCSMLHLCGSGTRLPALTVHVTPQKDGCFCEVCKKLVGYLD 420
Db 360 VDTYSSILSLLEEVSPELVCSMLHLCGSGTRLPALTVHVTPQKDGCFCEVCKKLVGYLD 419
Qy 421 RNLEKNSTKQETLAALKEGCSFLDPYQKQCDQFVAEYEPVLIETLVEMDPSFVCLKIG 480
Db 420 RNLEKNSTKQETLAALKEGCSFLDPYQKQCDQFVAEYEPVLIETLVEMDPSFVCLKIG 479
Qy 481 ACPSAHKPLLGTETKCIWGPSYWCNTETAACNAVEHCKRHWN 524
Db 480 ACPSAHKPLLGTETKCIWGPSYWCNTETAACNAVEHCKRHWN 523
RESULT 8
US-08-484-594A-2
; Sequence 2, Application US/08484594A
; Patent No. 5714459
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484.594A
; FILING DATE: 07-JUN-1995

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; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: MYELOS.002DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-484-594A-2

Query Match      98.9%; Score 2757.5; DB 1; Length 523;
Best Local Similarity 99.2%; Pred. No. 1.4e-239;
Matches 520; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 MYALFLASLLGAALAGPVGLGKCTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60
DB 1 MYALFLASLLGAALAGPVGLGKCTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKDNATEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
DB 61 LPCDICKDVVTAAGDMLKDNATEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
QY 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
DB 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
QY 181 PQDGRSPKQPKDGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGGMADI 240
DB 181 PQDGRSPKQPKDGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGGMADI 239
QY 241 CKNYISQYSEIAIQMMHMOPKEICALVGFCDVEKEMPQTLVPAKVASKNVIIPALELVE 300
DB 240 CKNYISQYSEIAIQMMHMOPKEICALVGFCDVEKEMPQTLVPAKVASKNVIIPALDLVD 299
QY 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCSKLPKSLSEECQEV 360
DB 300 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCSKLPKSLSEECQEV 359
QY 361 VDTYSSILSLILEVSPPELVCSMLHLCSTGTRLPALTVHTVTPKDGGFCEVCKKLVGLYD 420
DB 360 VDTYSSILSLILEVSPPELVCSMLHLCSTGTRLPALTVHTVTPKDGGFCEVCKKLVGLYD 419
QY 421 RNLEKNSTKQELIAALEKGCFLPDYQKQCDQFVAEYEPVLIELVEMDPSPFVCLKIG 480
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DB 480 ACPSAHKPLLGTEKICWGPSYWCQNTETAAQNAVEHCKRHVN 523
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RESULT 9

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US-09-076-258A-2
; Sequence 2, Application US/09076258A
; Patent No. 6559124
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED
; TITLE OF INVENTION: THEREFROM
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; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Blvd. 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,258A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,970
; FILING DATE: 28-OCT-97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/483,146
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: MYELOS.2DV1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-09-076-258A-2

Query Match      98.9%; Score 2757.5; DB 4; Length 523;
Best Local Similarity 99.2%; Pred. No. 1.4e-239;
Matches 520; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 MYALFLASLLGAALAGPVGLGKCTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60
DB 1 MYALFLASLLGAALAGPVGLGKCTRGSAVWCNQVKTASDCGAVKHCLQTVWNKPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKDNATEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
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QY 181 PQDGRSPKQPKDGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGGMADI 240
DB 181 PQDGRSPKQPKDGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGGMADI 239
QY 241 CKNYISQYSEIAIQMMHMOPKEICALVGFCDVEKEMPQTLVPAKVASKNVIIPALELVE 300
DB 240 CKNYISQYSEIAIQMMHMOPKEICALVGFCDVEKEMPQTLVPAKVASKNVIIPALDLVD 299
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Db 360 VDTYGSILSILLEVSPELVCSMLHLCSTRLPALTVHTQPKDGGFCEVCKLVGTLID 419
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Db 420 RNLEKNSTQETILALEKCSFLPDYPYQKQDOFVAEYEPVLIELVEMDPSFVCLKIG 479
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Db 480 ACPSAHKPLGTGKTCWGSYWCNTTAAQCNVAVHECHKRHVYN 523

RESULT 10
US-09-352-548-2
; Sequence 2, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431ei Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Saposin B
US-09-352-548-2

Query Match 15.5%; Score 431; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.4e-31; Mismatches 0; Indels 0; Gaps 0;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 GDVQCDCIQMVTDIQTAVRTNSTFVQALVHVKECDRLGPGMADICKNYISQYSEIAIQ 254
Db 1 GDVQCDCIQMVTDIQTAVRTNSTFVQALVHVKECDRLGPGMADICKNYISQYSEIAIQ 60

QY 255 MMHMOPKEICALVGFCEVK 275
Db 61 MMHMOPKEICALVGFCEVK 81

RESULT 11
US-08-584-671-15
; Sequence 15, Application US/08584671
; Patent No. 5910568
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESS: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/584,671
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/584,671
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; APPLICATION NUMBER: US/08/584,671

; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-08-584-671-15

Query Match 15.0%; Score 418.5; DB 2; Length 80;
Best Local Similarity 98.8%; Pred. No. 3.1e-30; Mismatches 0; Indels 1; Gaps 1;
Matches 80; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 128 PCEVCSALNLCESLQKHIAELNHQKLESNKIPELDMTEVVAFFMANIPLLLYPQDGPGRS 187
Db 1 PCEVC-ALNLCESLQKHIAELNHQKLESNKIPELDMTEVVAFFMANIPLLLYPQDGPGRS 59

QY 188 KPQPKNGDVCQDCIQMVTDI 208
Db 60 KPQPKNGDVCQDCIQMVTDI 80

RESULT 12
US-09-027-376-15
; Sequence 15, Application US/09027376
; Patent No. 6004586
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESS: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/027,376
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/584,671
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; APPLICATION NUMBER: US/08/584,671

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; TOPOLOGY: UNKNOWN
; US-09-027-376-15
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; Query Match 15.0%; Score 418.5; DB 3; Length 80;
; Best Local Similarity 98.8%; Pred. No. 3.1e-30;
; Matches 80; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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; QY 128 PGEVCSALNLCESLQKHIAELNHQKLESNKIPELDMTEVAVPFWANIPLLLYPDGPRS 187
; Db 1 PGEVC-ALNLCESLQKHIAELNHQKLESNKIPELDMTEVAVPFWANIPLLLYPDGPRS 59
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; QY 188 KPQPKDNGDVQDCIQMTDI 208
; Db 60 KPQPKDNGDVQDCIQMTDI 80
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; RESULT 13
; US-09-094-192-15
; Sequence 15, Application US/09094192
; Patent No. 6103483
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM TO EGG SURFACES AND PRO
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,192
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80
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; TOPOLOGY: UNKNOWN
; US-09-094-192-15
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; Query Match 14.9%; Score 415.5; DB 3; Length 80;
; Best Local Similarity 97.5%; Pred. No. 5.8e-30;
; Matches 79; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
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; QY 128 PGEVCSALNLCESLQKHIAELNHQKLESNKIPELDMTEVAVPFWANIPLLLYPDGPRS 187
; Db 1 PGEVC-ALNLCESLQKHIAELNHQKLESNKIPELDMTEVAVPFWANIPLLLYPDGPRS 59
;
; QY 188 KPQPKDNGDVQDCIQMTDI 208
; Db 60 KPQPKDNGDVQDCIQMTDI 80
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; RESULT 14
; US-08-100-247-3
; Sequence 3, Application US/08100247
; Patent No. 5571787
;
; GENERAL INFORMATION:
; APPLICANT: O'BRIEN, JOHN S.
; APPLICANT: KISHIMOTO, YASUO
; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
; CITY: NEWPORT BEACH
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,247
; FILING DATE: 19930730
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: O'BRIEN.002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; CLONE: SAPOSIN C
; US-08-100-247-3
;
; Query Match 14.8%; Score 412; DB 1; Length 80;
; Best Local Similarity 100.0%; Pred. No. 1.2e-29;
; Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 311 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVYTGSSILS 370
; Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQVVDVYTGSSILS 60
;
; QY 371 ILLEVPSPELVCSMLHLCSG 390
; Db 61 ILLEVPSPELVCSMLHLCSG 80
;
; RESULT 15
; US-08-483-146A-3
; Sequence 3, Application US/08483146A
; Patent No. 5696080
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Blvd. 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,146A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: MYELOS.002DV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-483-146A-3

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Query Match      14.8%; Score 412; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.2e-29;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      |||
Db      1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMKSLPKSLSECEWVDYTGSSILS 60

Qy      371 ILLEEVSPELVCSMLHLCSG 390
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Db      61 ILLEEVSPELVCSMLHLCSG 80

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Search completed: June 30, 2005, 11:38:06
Job time : 26 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2005, 11:26:11 ; Search time 42 Seconds
(without alignments)
1200.419 Million cell updates/sec

Title: US-09-743-684A-1
Perfect score: 2789
Sequence: 1 MYALFLASLIGALAGPVL.....NTETAACQNAVECKRHWVN 524

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR-79:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2777.5	99.6	527	1 SAHUP	saposin precursor
2	1996	71.6	554	1 A28716	saposin precursor
3	1937.5	69.5	557	1 JH0604	saposin precursor
4	511	18.3	965	2 T00207	P109 protein - sil
5	389	13.9	79	2 A49475	cerebroside sulfat
6	379	13.6	376	2 S02766	pulmonary surfacta
7	348.5	12.5	381	1 LNHUB	pulmonary surfacta
8	343	12.3	80	2 S21770	saposin-C - bovine
9	310	11.1	363	2 A29072	pulmonary surfacta
10	301.5	10.8	369	2 I46531	surfactant protein
11	261	9.4	81	2 A32026	glucosylceramide b
12	256.5	9.2	370	1 LNRBB	pulmonary surfacta
13	213	7.6	213	2 T46069	hypothetical prote
14	203.5	7.3	217	2 T48201	hypothetical prote
15	176.5	6.3	402	2 T15677	hypothetical prote
16	173.5	6.2	513	2 T09739	aspartic endopepti
17	171.5	6.1	506	2 F82253	hypothetical prote
18	165.5	5.9	506	2 T07915	probable aspartic
19	161.5	5.8	513	2 T11686	aspartic proteinas
20	161	5.8	428	2 S47096	cynarase (EC 3.4.2
21	161	5.8	474	2 T12049	cyprosin (EC 3.4.2
22	158.5	5.7	508	2 S19697	aspartic proteinas
23	156	5.6	314	2 T15674	hypothetical prote
24	155.5	5.6	292	2 T14446	aspartic proteinas
25	155.5	5.6	322	2 S41400	aspartic proteinas
26	154	5.5	496	2 JS0732	aspartic proteinas
27	153.5	5.5	509	2 JC7272	aspartic proteinas
28	145.5	5.2	205	2 B89567	protein T08A9.7 [i
29	143.5	5.1	1175	2 S52417	E-selectin ligand-

30	142.5	5.1	509	2 S49349	cyprosin (EC 3.4.2
31	142.5	5.1	509	2 S65516	oryzasin (EC 3.4.2
32	142.5	5.1	1948	2 S00485	gene 11-1 protein
33	141	5.1	508	2 D85056	probable aspartic
34	134	4.8	1927	2 G64585	cag pathogenicity
35	132.5	4.8	433	2 E96649	hypothetical prote
36	127.5	4.6	280	2 PC4080	aspartic proteinas
37	127.5	4.6	1142	2 A45031	cysteine-rich fibr
38	126.5	4.5	195	2 T15676	hypothetical prote
39	126.5	4.5	1819	2 A71928	cag island protein
40	126	4.5	506	2 S71591	aspartic proteinas
41	123.5	4.4	370	2 E96502	hypothetical prote
42	119	4.3	661	2 S67177	hypothetical prote
43	116.5	4.2	652	2 F85017	probable CHP-rich
44	116.5	4.2	707	2 T26218	hypothetical prote
45	116	4.2	975	2 E15422	rsec8 - rat (fragm
46	116	4.2	1357	2 B96696	protein Fin21.4 [i
47	115.5	4.1	1002	2 T30546	major surface glyco
48	115.5	4.1	3026	2 T28431	variant surface pr
49	115.5	4.1	3187	2 JC5837	364K Golgi complex
50	114.5	4.1	1216	2 A28821	1-phosphatidylinos
51	114	4.1	984	2 S14382	hypothetical prote
52	114	4.1	1051	2 JC4091	glycoprotein A - P
53	114	4.1	2297	2 AB2494	hypothetical prote
54	113.5	4.1	1317	2 T14595	polyprotein - maiz
55	113	4.1	2829	2 A42771	reticulocyte-bind
56	112.5	4.0	1014	2 T30545	major surface glyco
57	112.5	4.0	1953	2 T40642	probable helicase
58	112	4.0	1184	2 A55184	fibulin-2 precursor
59	112	4.0	1216	2 A28822	1-phosphatidylinos
60	112	4.0	1462	2 T11648	probable mitotic s
61	112	4.0	2541	2 T29340	hypothetical prote
62	111.5	4.0	380	2 T24678	hypothetical prote
63	111.5	4.0	1187	2 T18355	hypothetical prote
64	110.5	4.0	1013	2 B96544	hypothetical prote
65	110.5	4.0	1642	2 T08880	NMDA receptor-bind
66	110	3.9	774	2 JC2299	cell surface glyco
67	110	3.9	2218	2 B84683	hypothetical prote
68	109.5	3.9	1312	2 T30845	probable DNA repai
69	109	3.9	891	2 T32079	hypothetical prote
70	109	3.9	1557	2 T18412	lipid-binding prot
71	108.5	3.9	3507	2 T34513	hypothetical prote
72	108.5	3.9	3678	2 S28916	dyatrophin - mouse
73	108	3.9	3051	2 S42373	hypothetical prote
74	107.5	3.9	520	2 S35575	myosin heavy chain
75	107.5	3.9	835	1 Q0BEHA	BSLF1 protein - sa
76	107.5	3.9	1133	2 T13384	hypothetical prote
77	107.5	3.9	1173	1 A53430	1-phosphatidylinos
78	107.5	3.9	1234	2 T00363	hypothetical prote
79	107.5	3.9	3660	1 S02041	dyatrophin, muscle
80	107	3.8	1018	2 T37484	probable dna repai
81	107	3.8	1126	2 S49208	transmembrane prot
82	106.5	3.8	412	1 C37777	polyferredoxin 6x2
83	106.5	3.8	1350	2 S00647	finger protein - A
84	106	3.8	549	2 F71219	probable thermophi
85	106	3.8	941	2 T33032	hypothetical prote
86	106	3.8	1008	2 T30544	major surface glyco
87	106	3.8	1548	2 S34583	serine proteinase
88	106	3.8	2672	2 A48126	translation activa
89	106	3.8	2823	2 F87908	hypothetical prote
90	106	3.8	2823	2 T23064	hypothetical prote
91	106	3.8	3102	2 T43291	laminin alpha chai
92	105.5	3.8	764	2 S09318	transcription fact
93	105.5	3.8	764	2 A40439	UBF transcription
94	105.5	3.8	765	2 S22314	transcription fact
95	105.5	3.8	860	2 A96717	unknown protein, 4
96	105.5	3.8	869	2 F97126	mismatch repair pr
97	105	3.8	473	2 T04799	hypothetical prote
98	105	3.8	474	1 VYHUD	vitamin D-binding
99	105	3.8	1134	2 T20332	hypothetical prote
100	104.5	3.7	572	2 T27869	sphingomyelin phos

ALIGNMENTS

RESULT 1

SAHUP

N;Alternative names: cerebroside sulfate activator protein; co-beta-glucosidase; component ein (SAP); sphingolipid activator protein A2; sulfatide sulfatase activator protein
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1992 #sequence revision 17-Nov-1995 #text change 09-Jul-2004
 C;Accession: JX0061; A57368; A42003; B42003; C42003; D42003; A30367; S34740; S36140; S360226; I37265; I37264
 J; Nakano, T.; Sandhoff, K.; Christomanou, H.; Suzuki, K.
 R; Biochem. 105, 152-154, 1989
 A;Title: Structure of full-length cDNA coding for sulfatide activator, a Co-beta-glucosidase
 A;Reference number: JX0061; MUID:89255151; PMID:2498298
 A;Accession: JX0061
 A;Molecule type: mRNA
 A;Residues: 1-527 <NAK>
 A;Cross-references: UNIPROT:P07602; GB:D00422; NID:g220063; PIDN:BA00321.1; PID:g220064
 A;Note: alternative splice form 1
 A;Accession: A57368
 A;Molecule type: mRNA
 A;Residues: 1-259,263-527 <NA2>
 A;Cross-references: GB:J03015; GB:J03086; NID:g337755; PIDN:AAB59494.1; PID:g337756
 A;Note: alternative splice form 2
 R;Rorman, E.G.; Scheinker, V.; Grabowski, G.A.
 Genomics 13, 312-318, 1992
 A;Title: Structure and evolution of the human prosaposin chromosomal gene.
 A;Reference number: A42003; MUID:92307663; PMID:1612590
 A;Accession: A42003
 A;Molecule type: DNA
 A;Residues: 50-140 <ROR>
 A;Cross-references: GB:M86181
 A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107236)
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 A;Residues: 185-259,263-276 <RO2>
 A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107237)
 A;Accession: C42003
 A;Molecule type: DNA
 A;Residues: 305-393 <RO3>
 A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107238); sequence inc
 A;Accession: D42003
 A;Molecule type: DNA
 A;Residues: 399-487 <RO4>
 A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107239); sequence inc
 R;Rorman, E.G.; Grabowski, G.A.
 Genomics 5, 486-492, 1989
 A;Title: Molecular cloning of a human co-beta-glucosidase cDNA: evidence that four sphin
 A;Reference number: A30367; MUID:90129043; PMID:2515150
 A;Accession: A30367
 A;Molecule type: mRNA
 A;Residues: 1-259,263-527 <RO5>
 A;Cross-references: GB:J03077; NID:g183230; PIDN:AAA52560.1; PID:g183231
 A;Note: alternative splice form 2
 R;Hiraiwa, M.; O'Brien, J.S.; Kishimoto, Y.; Galdzicka, M.; Fluharty, A.L.; Ginns, E.I.; Arch. Biochem. Biophys. 304, 110-116, 1993
 A;Title: Isolation, characterization, and proteolysis of human prosaposin, the precursor
 A;Reference number: S34740; MUID:93311991; PMID:8323276
 A;Accession: S34740
 A;Molecule type: protein
 A;Residues: 17-24;165-172;180-189;301-305 <HIR>
 R;Tyynelae, J.; Palmer, D.N.; Baumann, M.; Haltia, M.
 FEBS Lett. 330, 8-12, 1993
 A;Title: Storage of saposins A and D in infantile neuronal ceroid-lipofuscinosis.
 A;Reference number: S36140; MUID:93380576; PMID:8370464
 A;Accession: S36140
 A;Molecule type: protein
 A;Residues: 'XX',62,'X',64-65,'X',67-79,'X',81-84 <TYV>
 A;Note: saposin A
 A;Accession: S36141

A;Molecule type: protein
 A;Residues: 'XXX',413-414,'X',416-428,'X',430-434 <TY2>
 A;Note: saposin D
 R;Holtzschmidt, H.; Sandhoff, K.; Kwon, H.Y.; Harzer, K.; Nakano, T.; Suzuki, K.
 J. Biol. Chem. 266, 7556-7560, 1991
 A;Title: Sulfatide activator protein. Alternative splicing that generates three mRNAs an
 A;Reference number: S36988; MUID:91210267; PMID:2019586
 A;Accession: S36988
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-240,'S',242-527 <HOL>
 A;Cross-references: EMBL:M60255; NID:g337759; PIDN:AAA36594.1; PID:g337760
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
 A;Note: cerebroside sulfate activator protein mutant MU-9; corresponds to alternative sp
 A;Accession: S36989
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-240,'S',242-259,263-527 <HO2>
 A;Cross-references: EMBL:M60257; NID:g337764; PIDN:AAA36595.1; PID:g337765
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
 A;Note: cerebroside sulfate activator protein mutant MU-0; corresponds to alternative sp
 A;Accession: S36990
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-240,'S',242-259,261-527 <HO3>
 A;Cross-references: EMBL:M60258; NID:g337766; PIDN:AAA36596.1; PID:g337767
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
 A;Note: cerebroside sulfate activator protein mutant MU-6; corresponds to alternative sp
 R;Kondo, K.; Hinenio, T.; Sano, A.; Kakimoto, Y.
 Biochem. Biophys. Res. Commun. 181, 286-292, 1991
 A;Title: Isolation and characterization of prosaposin from human milk.
 A;Reference number: PS0330; MUID:92068206; PMID:1958198
 A;Accession: PS0330
 A;Molecule type: protein
 A;Residues: 17-24,'X',26 <KON>
 A;Experimental source: milk
 R;Kretz, K.A.; Carson, G.S.; Morimoto, S.; Kishimoto, Y.; Fluharty, A.L.; O'Brien, J.S.
 Proc. Natl. Acad. Sci. U.S.A. 87, 2541-2544, 1990
 A;Title: Characterization of a mutation in a family with saposin B deficiency: a glycosy
 A;Reference number: A35985; MUID:90207231; PMID:2320574
 A;Accession: A35985
 A;Molecule type: mRNA
 A;Residues: 213-221 <KRE>
 A;Cross-references: GB:M32221
 A;Accession: B35985
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-259,263-527 <KR2>
 A;Cross-references: GB:M32221; NID:g337761; PIDN:AAA60303.1; PID:g337762
 A;Experimental source: Lymphoblast
 A;Accession: C35985
 A;Molecule type: mRNA
 A;Residues: 213-216,'I',218-221 <KR3>
 A;Note: sequence from patients with activator-deficient metachromatic leukodystrophy; th
 R;Fuerst, W.; Schubert, J.; Machleidt, W.; Meyer, H.E.; Sandhoff, K.
 Eur. J. Biochem. 192, 709-714, 1990
 A;Title: The complete amino-acid sequences of human ganglioside GM2 activator protein an
 A;Reference number: S13195; MUID:91006165; PMID:2209618
 A;Accession: S13196
 A;Molecule type: protein
 A;Residues: 195-259,263-277 <FUE>
 R;Morimoto, S.; Martin, B.M.; Yamamoto, Y.; Kretz, K.A.; O'Brien, J.S.; Kishimoto, Y.
 Proc. Natl. Acad. Sci. U.S.A. 86, 3389-3393, 1989
 A;Title: Saposin A: second cerebrosidase activator protein.
 A;Reference number: A32784; MUID:89240739; PMID:2717620
 A;Accession: A32784
 A;Molecule type: protein
 A;Residues: 60-84;86-107;109-119;125-134 <MOR>
 R;O'Brien, J.S.; Kretz, K.A.; Dewji, N.; Wenger, D.A.; Esch, F.; Fluharty, A.L.
 Science 241, 1098-1101, 1988
 A;Title: Coding of two sphingolipid activator proteins (SAP-1 and SAP-2) by same genetic
 A;Reference number: A41240; MUID:88321660; PMID:2842863
 A;Accession: A41240

A:Molecule type: mRNA
A:Residues: 'GSR',18-259,263-299,'D',301-302,'D',304-527 <OAB>
A:Cross-references: GB:J03086
R:Dewji, N.N.; Wenger, D.A.; O'Brien, J.S.
Proc. Natl. Acad. Sci. U.S.A. 84, 8652-8656, 1987
A:Title: Nucleotide sequence of cloned cDNA for human sphingolipid activator protein 1 p
A:Reference number: S02289; MUID:88068647; PMID:2825202
A:Accession: S02289
A:Status: significant sequence differences
A:Molecule type: mRNA
A:Cross-references: EMBL:J03015
A:Note: this sequence corrected by A41240
A:Note: part of this sequence, including the amino end of the mature protein, was determ
R:Kleinschmidt, T.; Christomanou, H.; Braunitzer, G.
Biol. Chem. Hoppe-Seyler 369, 317-328, 1988
A:Title: Complete amino-acid sequence of the naturally occurring A(2) activator protein
A:Reference number: S02028; MUID:89207118; PMID:3242555
A:Accession: S02028
A:Molecule type: protein
A:Residues: 195-259,263-276 <KLB>
R:Fuerst, W.; Machleidt, W.; Sandhoff, K.
Biol. Chem. Hoppe-Seyler 369, 317-328, 1988
A:Title: The precursor of sulfatide activator protein is processed to three different pr
A:Reference number: S00813; MUID:89000190; PMID:3048308
A:Accession: S00813
A:Molecule type: protein
A:Residues: 410-487 <F02>
R:Kleinschmidt, T.; Christomanou, H.; Braunitzer, G.
Biol. Chem. Hoppe-Seyler 368, 1571-1578, 1987
A:Title: Complete amino-acid sequence and carbohydrate content of the naturally occurin
A:Reference number: S00226; MUID:88163077; PMID:3442600
A:Accession: S00226
A:Molecule type: protein
A:Residues: 314-393 <KL2>
R:Vaccaro, A.M.; Salvioli, R.; Barca, A.; Tatti, M.; Ciaffoni, F.; Maras, B.; Siciliano,
J. Biol. Chem. 270, 9953-9960, 1995
A:Title: Structural analysis of saposin C and B. Complete localization of disulfide brid
A:Reference number: A57297; MUID:95247790; PMID:7730378
A:Contents: annotation; disulfide bonds; glycosylation
R:Holtshmidt, H.; Sandhoff, K.; Fuerst, W.; Kwon, H.Y.; Schnabel, D.; Suzuki, K.
FEBS Lett. 280, 267-270, 1991
A:Title: The organization of the gene for the human cerebroside sulfate activator protei
A:Reference number: I37264; MUID:91192146; PMID:2013321
A:Accession: I37265
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 59-125 <RES>
A:Cross-references: EMBL:X57107; NID:G30234; PIDN:CAA40391.1; PID:G30235
A:Accession: I37264
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 307-516 <RE2>
A:Cross-references: EMBL:X57108; NID:G30232; PIDN:CAA40392.1; PID:G1565257
A:Note: sequence revised relative to PID:G30233 (corrected coding region)
C:Genetics:
A:Gene: GDB:PSAP; GLBA
A:Cross-references: GDB:I20366; OMIM:176801
A:Map position: 10q22.1-10q22.1
A:Introns: 83/3; 338/3; 401/1; 453/3; 480/3
A:Note: defects in this gene may cause variant Gaucher disease, variant Tay-Sachs disease
A:Note: list of introns is incomplete
Query Match 99.6%; Score 2777.5; DB 1; Length 527;
Best Local Similarity 99.4%; Pred. No. 7.7e-176;
Matches 524; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 MYALFLLASLLGAALAGPVLGKECTRGSAVQCNVKTASDCGAVKHCLQTWNKPTVKS 60
DB 1 MYALFLLASLLGAALAGPVLGKECTRGSAVQCNVKTASDCGAVKHCLQTWNKPTVKS 60
QY 61 LPDCICKOVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNNSASCKEIVDSYLPVILDI 120
DB 61 LPDCICKOVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNNSASCKEIVDSYLPVILDI 120

QY 121 IKGMSRPGVCSALNLCESLQKHLAEHLNHOQLESNKIPELDMTEVVAPFMANIPLLY 180
DB 121 IKGMSRPGVCSALNLCESLQKHLAEHLNHOQLESNKIPELDMTEVVAPFMANIPLLY 180
QY 191 PQDGRSPKQPKDNGDVQCDCIQMVTDIQTAVRTNSTFQALVEHVKECDRLGPGMADI 240
DB 191 PQDGRSPKQPKDNGDVQCDCIQMVTDIQTAVRTNSTFQALVEHVKECDRLGPGMADI 240
QY 241 CKNYISQYSEIAIQMMHMH---QPKIEICALVGFCDVEKEMPQTLVPAKVASKNVIPA 297
DB 241 CKNYISQYSEIAIQMMHMH---QPKIEICALVGFCDVEKEMPQTLVPAKVASKNVIPA 300
QY 298 LVEPIKGEHVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAPDKVCSKLPKLSBEC 357
DB 301 LVEPIKGEHVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDAPDKVCSKLPKLSBEC 360
QY 358 QEVVDYTGSSITSLILREVSPELVCSMLHLCSGTRLPALTVHVTPQDKGGFCEVCKLVG 417
DB 361 QEVVDYTGSSITSLILREVSPELVCSMLHLCSGTRLPALTVHVTPQDKGGFCEVCKLVG 420
QY 418 YLDRLNLEKNSTKQETLAALKEGCSFLPDYQKQCDQFVAEYEPVLIIEILVEVMDPSFVCL 477
DB 421 YLDRLNLEKNSTKQETLAALKEGCSFLPDYQKQCDQFVAEYEPVLIIEILVEVMDPSFVCL 480
QY 478 KIGACPSAHKPLLGTEKCIWGPSYWCQNTETAACQNAVEHCCKRHVN 524
DB 481 KIGACPSAHKPLLGTEKCIWGPSYWCQNTETAACQNAVEHCCKRHVN 527
RESULT 2
A28716
N:Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; component
ein (SAP); sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulfata
N:Contains: prosaposin; saposin A; saposin B; saposin C; saposin D
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A28716
R:Collard, M.W.; Sylvestre, S.R.; Tauruta, J.K.; Griswold, M.D.
Biochemistry 27, 4557-4564, 1988
A:Title: Biosynthesis and molecular cloning of sulfated glycoprotein 1 secreted by rat
A:Reference number: A28716; MUID:89000647; PMID:3048385
A:Accession: A28716
A:Molecule type: mRNA
A:Residues: 1-554 <COL>
A:Cross-references: UNIPROT:P10960; GB:M19936; NID:G206904; PIDN:AAA42136.1; PID:G206905
A:Note: parts of this sequence, including the amino end of the mature protein, were deter
C:Function:
A:Description: saposins bind sphingolipids, form hydrophilic complexes and make them acc
A:Pathway: sphingolipid catabolism
A:Note: saposins A and C (SAP-2) activate hydrolysis of glucocerebroside by beta-glucosy
A:Note: saposin B (SAP-1) activates hydrolysis of galactocerebroside sulfate by arylsul
A:Note: saposin D activates hydrolysis of sphingomyelin by sphingomyelin phosphodiester
C:Superfamily: saposin; saposin repeat homology
C:Keywords: alternative splicing; glycoprotein; lysosomal storage disease; lysosome; sph
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-554/Product: prosaposin #status predicted <PRO>
F:55-148/Domain: saposin repeat homology <SAP1>
F:160-143/Product: saposin A #status predicted <SAPA>
F:189-280/Domain: saposin repeat homology <SAP2>
F:194-273/Product: saposin B #status predicted <SAB1>
F:306-397/Domain: saposin repeat homology <SAP3>
F:310-389/Product: saposin C #status predicted <SAPC>
F:431-522/Domain: saposin repeat homology <SAP4>
F:437-514/Product: saposin D #status predicted <SAPD>
F:63-138,66-132,94-106,439-512,442-506,470-481/Disulfide bonds: #status predicted
F:80,214,331,456/Binding site: carbohydrate (asn) (covalent) #status predicted
F:197-270,200-264,229-240,314-387,317-381,345-355/Disulfide bonds: #status predicted
Query Match 71.6%; Score 1996; DB 1; Length 554;
Best Local Similarity 66.3%; Pred. No. 3.2e-124;
Matches 368; Conservative 77; Mismatches 78; Indels 32; Gaps 3;

Qy 1 MYALFLLASLGAALAGPVLGKECTRGSAVWCONVKTASDCGAVKHCLQTVWVKPTVKS 60
Db 1 MYALALLASLVLATLTSPVQPKTCGSGSAVVCRDVKTAVDCRAVKGHCQQVWWSKPTAKS 60
Qy 61 LPCDICKDVVTAAGDMLKDNATEEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKVVTVEAGNLLKDNATEEBEILVYLEKTCWIIHDSLSASCKEIVDSYLPVILDM 120
Qy 121 IKGMSRPGVCSALNLCESLOKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
Db 121 IKGMSNPGVCSALNLCQSLQELAEQN-QRQLESNKIPEVDLARVVAPFMSNIPLLLY 179
Qy 181 PQDGRSKPQPKNGDVCQDCIQMVTDTQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
Db 180 PQDRPRSOPQPKANEDVCQCMKLVTDIQTAVRTNSSFVQGLVDHVKEEDCDRLGPGVSDI 239
Qy 241 CKNYISQYSEITAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPAELAVE 300
Db 240 CKNYVDQYSEVAVQMMHMQPKEICVMVGFCDVEKVRPMRTLVPAATEAIKNILPALELTD 299
Qy 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELTDAFDKWCCKLPKSLSEECQEV 360
Db 300 PYEQDVIAQNVIFCQVCQLVMRKLSELIINNATEELIKGLSKACSLLPAPASTKCOEV 359
Qy 361 VDTYSSILSILLEVSPPELVCSMLHLCGSG-----TRLP- 394
Db 360 LVTFGPSLLDVLMEVWNFILCGVISLCSANPNLVGTLEQPAALIVSALPKPEAPPKQPE 419
Qy 395 -----ALTVHVTQPKDGGFCVCKKLVGYLDRLNLEKSTKQEIILAALEKGCFLPDPYQK 449
Db 420 EPKQSAALRAHVPPQKNGGFCVCKKLVLYLEHNLEKSTKEEILAALEKGCFLPDPYQK 479
Qy 450 QCDQFVAYEYEPVLBIILVEVMDPSFVCLIKIGACPSAHKPLLGTEKICWGPSYWCNTETA 509
Db 480 QCDEFVAYEYEPVLBIILVEVMDPSFVCKSIGVCFPSAYKLLLGTEKICWVGWPGYWCQNSETA 539
Qy 510 AQCNNAVEHCKRHWVN 524
Db 540 ARCNNAVDHCKRHWVN 554
RESULT 3
JH0604
saposin precursor - mouse
N:Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; component
ein (SAP); sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulfata
N:Contains: prosaposin; saposin A; saposin B; saposin C; saposin D
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JH0604
R:Tsuda, M.; Sakiyama, T.; Endo, H.; Kitagawa, T.
Biochem. Biophys. Res. Commun. 184, 1266-1272, 1992
A:Title: The primary structure of mouse saposin.
A:Reference number: JH0604; MUID:92272718; PMID:1590788
A:Accession: JH0604
A:Molecule type: mRNA
A:Residues: 1-557 <TSU>
A:Cross-references: UNIPROT:061207; GB:S36200; NID:g249386; PIDN:AAB22175.1; PID:g249387
A:Experimental source: liver
C:Function:
A:Description: saposins bind sphingolipids, form hydrophilic complexes and make them acc
A:Pathway: sphingolipid catabolism
A>Note: saposins A and C (SAP-2) activate hydrolysis of glucocerebroside by beta-glucosy
A>Note: saposin B (SAP-1) activates hydrolysis of galactocerebroside sulfate by arylsul
A>Note: saposin D activates hydrolysis of sphingomyelin by sphingomyelin phosphodiester
C:Superfamily: saposin; saposin repeat homology
C:Keywords: alternative splicing; glycoprotein; lysosomal storage disease; lysosome; sph
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-557/Product: prosaposin #status predicted <PRO>
F:55-148/Domain: saposin repeat homology <SAP1>
F:60-143/Product: saposin A #status predicted <SAPA>
F:189-283/Domain: saposin repeat homology <SAP2>

F:194-276/Product: saposin B #status predicted <SAB1>
F:309-400/Domain: saposin repeat homology <SAP3>
F:313-392/Product: saposin C #status predicted <SAPC>
F:434-525/Domain: saposin repeat homology <SAP4>
F:440-517/Product: saposin D #status predicted <SAPD>
F:63-138,66-132,94-106,197-273,200-267,229-240,317-390,320-384,348-359,442-515,445-509,4
F:80,214,334,379,459/Binding site: carbohydrate (Asn) #status predicted
Query Match 69.5%; Score 1937.5; DB 1; Length 557;
Best Local Similarity 63.6%; Pred. No. 2.4e-120; Indels 35; Gaps 3;
Matches 355; Conservative 77; Mismatches 91;
Qy 1 MYALFLLASLGAALAGPVLGKECTRGSAVWCONVKTASDCGAVKHCLQTVWVKPTVKS 60
Db 1 MYALALLASLVLATLTSPVQPKTCGSGSAVVCRDVKTAVDCRAVKGHCQQVWWSKPTAKS 60
Qy 61 LPCDICKDVVTAAGDMLKDNATEEBEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKVVTVEAGNLLKDNATQBEILHYLEKTCWIIHDSLSASCKEIVDSYLPVILDM 120
Qy 121 IKGMSRPGVCSALNLCESLOKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
Db 121 IKGMSNPGVCSALNLCQSLQELAEQN-QRQLESNKIPEVDLARVVAPFMSNIPLLLY 179
Qy 181 PQDGRSKPQPKNGDVCQDCIQMVTDTQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
Db 180 PQDRPRSOPQPKANEDVCQCMKLVSDVQTAVRTNSSFVQGLVDHVKEEDCDRLGPGVSDI 239
Qy 241 CKNYISQYSEITAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPAELAVE 297
Db 240 CKNYVDQYSEVAVQMMHMQPKEICVLVAGFCNEVKRPMRTLVPAATEAIKNILPALE 299
Qy 298 LVEPIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELTDAFDKWCCKLPKSLSEEC 357
Db 300 MMDPYEQLVQAHNVILCQTCQFVWNNKSELIIVNNAEELLVKGLSNACGVLDPDPARTKC 359
Qy 358 QEVVDYTSILSILLEVSPPELVCSMLHLCGSG----- 390
Db 360 QEVVGTGPSLLDIFIHEVWNPSSLCGVLCAARPELVEALQPAPAIVSALLKEPTPK 419
Qy 391 -----TRLPALTVHVTQPKDGGFCVCKKLVGYLDRLNLEKSTKQEIILAALEKGCFLPDP 446
Db 420 QPAQPKQSAALPAHVPPQKNGGFCVCKKLVLYLEHNLEKSTKEEILAALEKGCFLPDP 479
Qy 447 YQKCDQFVAYEYEPVLBIILVEVMDPSFVCLIKIGACPSAHKPLLGTEKICWGPSYWCNT 506
Db 480 YQKCDQFVAYEYEPVLBIILVEVMDPSFVCKSIGVCFPSAYKLLLGTEKICWVGWPGYWCQNM 539
Qy 507 ETAAQCNNAVEHCKRHWVN 524
Db 540 ETAAACNNAVDHCKRHWVN 557
RESULT 4
T00207
P109 protein - silkworm
C:Species: Bombyx mori (silkworm)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C:Accession: T00207
R:Tambunan, J.; Chang, P.K.; Li, H.; Natori, M.
Gene 212, 287-293, 1998
A:Title: Molecular cloning of a cDNA encoding a silkworm protein which contains the cons
A:Reference number: Z14124; MUID:98278844; PMID:9611271
A:Accession: T00207
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-965 <TAM>
A:Cross-references: UNIPROT:O15997; EMBL:AB008449; NID:g2575864; PIDN:BAA23126.1; PID:g2
F:778-870/Domain: saposin repeat homology <SAP3>
Query Match 18.3%; Score 511; DB 2; Length 965;
Best Local Similarity 24.6%; Pred. No. 7.1e-26;
Matches 139; Conservative 104; Mismatches 229; Indels 94; Gaps 18;


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Query Match          12.5%; Score 348.5; DB 1; Length 381;
Best Local Similarity 21.6%; Pred. No. 1.2e-15;
Matches 111; Conservative 72; Mismatches 171; Indels 161; Gaps 16;

QY      2 YALFLIASILGAALGPVLGLKECTRGSAVWQNVKTASDCGAVKHCLQTVNKNKPTVKSL 61
DB      9 WLLLLPTLCGPQTAAWTTSSLIACAQPFQWQSLEQALQCRALGHCLQAVWGHVGADDL 68

QY     62 PCDICDVVTAAGMDLKNATBEEIIVLYLEKTCMDLKPKNMSASCKEIVDSYLPVLIDII 121
DB     69 -COECEDIIVHLNKAKEALFQDTWRFKELEQECNVLPPLKLLMPQCQNVLDYDFPLVIDYF 127

QY    122 KGMSPRGVCSALNLCESLQKHLABELNHQKLESNKIPELDMTEVVAPPMANIPLLLYP 181
DB    128 QNQTDSNG-ICMHLGLCKSRQ----- 147

QY    182 QDGPRSKPOPKONGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGWADIC 241
DB    148 -----PEPEQ----- 158

QY    242 KNYISQYSEIATQMMHMHQPKICALVGFCEVKEMPMOTLVPKAVSKNNVIPALELVEP 301
DB    159 -----PLPK-----PLRDPDPLDLLDKLVLPVLP--GA 184

QY    302 IKKHEVPAKSDV-----YCEVCEFLVKEVTKLIDNNKTEKEILDADFQKCSKLPK 351
DB    185 LQARPGPHQTDLSEQOFFPIPLPYCWLCLRALIKRIQAMIPKG-----ALRVAVAQVCRVPL 240

QY    352 SLSEECQEVVDYTGSSILSILEEVSPELVCSMLHLS-----GTRLPALTVAHVTPQKDG 406
DB    241 VAGGICOCALERYSVILLDTLLGRMLPQLVCLVLFLCSMDSDSAGPRSP---TGEWLPRDS 297

QY    407 GFCEVCKLVGLVLDRLNLEKNSTKQETLAALKEGC--SFLPDPYQKQCDQFVASEYEPVLIE 464
DB    298 E-CHLCNST-----TQAGNSEQALPQAMLQACVGSWLD---REKCKQFVEQHTQLLT 348

QY    465 ILVENVDPFSVCLIKIGACPSAHKPLLGTEKCIWGP 499
DB    349 LVPRGWDATTCQALGVCGTMSPL----QCIIHP 379

RESULT 8
S21770
saposin-C - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S21770
R:Sano, A.; Mizuno, T.; Kondoh, K.; Hineno, T.; Ueno, S.; Kakimoto, Y.; Morita,
Biochim. Biophys. Acta 1120, 75-80, 1992
A:Title: Saposin-C from bovine spleen; complete amino acid sequence and relation
A:Reference number: S21770; MUID:92207994; PMID:1554743
A:Accession: S21770
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-80 <SAN>
C:Superfamily: saposin; saposin repeat homology

Query Match          12.3%; Score 343; DB 2; Length 80;
Best Local Similarity 79.7%; Pred. No. 3.7e-16;
Matches 63; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY     311 SDVYCVBCEFLVKEVTKLIDNNKTEKEILDAPKMGSKLPKSLSEECQEVVDYTGSSILS 370
DB     1 ADYCVQCFVKEVAKLIDNNKTEKEILHALDKVCSKLPKSLAEQCEQEVVDYTGSSILS 60

QY     371 ILLEEVSPELVCSMLHLS 389
DB     61 ILLDEASPELVCSMLHLS 79

RESULT 9
A29072
pulmonary surfactant protein SP 18 precursor - dog (fragment)

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Db 3 VTCKACEYVVKVMBELIDNNRTEKIIHALDSVCALLPESVSEQVVDVYGDIVALL 62
QY 373 LEEVSPVLVCSMLHLIC 388
Db 63 LOEMSPVLVCSLGLIC 78
RESULT 12
LNRRBB
pulmonary surfactant protein B precursor - rabbit
N:Alternate names: pulmonary surfactant-associated protein-B
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: A32421
R:Xu, J.; Richardson, C.; Ford, C.; Spencer, T.; Li-Juan, Y.; Mackie, G.; Hammond, G.; F
Biochem. Biophys. Res. Commun. 160, 325-332, 1989
A:Title: Isolation and characterization of the cDNA for pulmonary surfactant-associated
A:Reference number: A32421; MUID:89228033; PMID:2469419
A:Accession: A32421
A:Molecule type: mRNA
A:Residues: 1-370 <XU>
A:Cross-references: UNIPROT:P15285; GB:M24901; NID:q165707; PIDN:AAA31466.1; PID:q165708
A:Note: the authors translated the codon CCG for residue 184 as Arg and CAG for residue
C:Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers t
C:Superfamily: pulmonary surfactant protein B; saposin repeat homology
C:Keywords: alveolar proteinosis; gaseous exchange; glycoprotein; lipoprotein; lung; pul
F:1-21/Domain: signal sequence #status predicted <SIG>
F:122-184/Domain: propeptide #status predicted <PRO>
F:162-154/Domain: saposin repeat homology <SAP1>
F:184-271/Domain: saposin repeat homology <SAP2>
F:185-263/Product: pulmonary surfactant protein B, 9K form #status predicted <SP9>
F:185-246/Product: pulmonary surfactant protein B, 6K form #status predicted <SP6>
F:280-365/Domain: saposin repeat homology <SAP3>
F:300/Binding site: carbonylate (Asn) (covalent) #status predicted
Query Match 9.2%; Score 256.5; DB 1; Length 370;
Best Local Similarity 20.7%; Pred. No. 1.3e-09;
Matches 108; Conservative 63; Mismatches 165; Indels 185; Gaps 20;
QY 4 LFLASLIGALAGVILGKECTRGSAVWCQNVKTASDCGAVKHCLQTVWKNPTVKSILPC 63
Db 12 LLLLPTLCGPGTAVVWATSPACAOQPFWCOSLEQALGHCLQEVWGHVGADDL-C 70
QY 64 DICKDVVTAAGDMLKDNATEEILVYLEKTDWLPKPNMSASCKEIVDSYLPVILDIKG 123
Db 71 QECQDIVNLTWTKREALFQDTIRKFLHEHCDVLPKLVLVQCHHVDVYFPLTIYFQS 130
QY 124 EMSRPEGVCSALNLCESLQKHLAELNHQKLESNKIPBLDMTEVVVAPFWANIPLLLYPQD 183
Db 131 QINAKA-ICQHLGLCQ-----PGSPEPLD---PLPKLVLPDLL---G 167
QY 184 GPRSPQPKNDGVQCDCIQWTDIQTAVRTNSTFQALVHVHEECDRLGFGMADICKN 243
Db 168 ALPAKPGP----- 175
QY 244 YISQYSEIAIQMMHWQPKIECALVGFCDVEKEMPQTLVPAKVASKNVIPALELVEPIK 303
Db 176 -----HTQ-----DUSAQFPPIPLP----- 190
QY 304 KHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILD-AFDKMCCKLPKSLSEECQEVVD 362
Db 191 -----LCWLCTLLKRIQAMI-----PKGVLAMAVAQVCHVPLVVGIGICQCLAE 235
QY 363 TYGSSILILLIEVSPVLVCSMLHLIC-----GTRLPALTVHVTO--PKDGGFCEVCKL 415
Db 236 RYTVILLEVLLGHVLPQLVCGVLRCSSVDISGVQVPTTLEALPGEWLPQDPE-CRLCMNV 294
QY 416 VGYLDRNLEKNSTKEILAA-----LEKGCSPLPDPYQKQDOFVAEYEPVLIETLVEVM 470
Db 295 TQQA-RNISEQTRPAVTHACLSQLDK-----QECQFVAHAAP-----AA 335
QY 471 DPSFVCLKIGACPSAHKPLLGE-----KCIWGPSY 501

Db 336 EPAVQGL---GCP---RNLPQEGRVVATLSPLOCIQSPHF 370
RESULT 13
T46069
hypothetical protein T18N14.110 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46069
R:Deiseny, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23013
A:Accession: T46069
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-213
A:Cross-references: UNIPROT:Q9SCTS; EMBL:AL132968
A:Experimental source: cultivar Columbia; BAC clone T18N14
C:Genetics:
A:Map position: 3
A:Introns: 31/1; 80/3; 146/3; 166/3
A:Note: T18N14.110
Query Match 7.6%; Score 213; DB 2; Length 213;
Best Local Similarity 29.7%; Pred. No. 4.9e-07;
Matches 57; Conservative 35; Mismatches 90; Indels 10; Gaps 6;
QY 292 VIPALELVEPIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDADFDMCKSLPK 351
Db 18 VSDARSFVDSITSEKVSNKEDV-CTLCSEYVTDALSYLEKNVTQAEIIEDLHRCSQL-R 75
QY 352 SLSECCQVWDYTGSSILILLEVSPVLVCSMLHLCSGTELPALTVHVTPQKGGFCEV 411
Db 76 GYSQQCSLVDYV-VPLFFLOLESFQPHYFCRNNLCG--KVVALVEEARQDS-----CGV 128
QY 412 CKKLVGVLDRNLERNSTKQETLAALKEGCSFLPDYQKQCFVAEYEPVLIETLVEYMD 471
Db 129 CHRTVSEILIKQDPDQTDIVELLIKGCKSLKN-YEKCKTLYFEYGLIIVNAEFLV 187
QY 472 PSFVCLKIGACP 483
Db 188 KNDVCTLLRACF 199
RESULT 14
T48201
hypothetical protein T20L15.70 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T48201
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24488
A:Accession: T48201
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-217 <BEV>
A:Cross-references: UNIPROT:Q9LZW6; EMBL:AL162351
A:Experimental source: cultivar Columbia; BAC clone T20L15
C:Genetics:
A:Map position: 5
A:Introns: 30/1; 79/3; 146/3; 166/3
A:Note: T20L15.70
Query Match 7.3%; Score 203.5; DB 2; Length 217;
Best Local Similarity 27.8%; Pred. No. 2.1e-06;
Matches 52; Conservative 40; Mismatches 82; Indels 13; Gaps 7;
QY 298 LVEPIKK-HEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDADFDMCKSLPKSLSEE 356
Db 25 LLEPFESAHD-----DNQVCELCDKYVTLVDYLDQYDNQNELVEALHISCQIP-PLKKQ 79

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2005, 11:25:30 ; Search time 178 Seconds
(without alignments)
1507.469 Million cell updates/sec

Title: US-09-743-684A-1
Perfect score: 2789
Sequence: 1 MYALFLASLLGALAGVL.....NTETAAQCNAVECHKRHVWN 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
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2	2782	99.7	524	2 Q6IBQ6
3	2425.5	87.0	525	1 SAP_BOVIN
4	1996	71.6	554	1 SAP_RAT
5	1982.5	71.1	553	2 Q6P7A4
6	1950	69.9	554	2 Q8BFQ1
7	1938.5	69.5	557	1 SAP_MOUSE
8	1679.5	60.2	518	1 SAP_CHICK
9	1442	51.7	512	2 Q7SY70
10	1429	51.2	518	2 Q642S6
11	1414	50.7	520	2 Q8UVZ4
12	1411	50.6	520	2 Q6PH48
13	1411	50.6	520	2 Q6P3G7
14	1343	48.2	522	2 Q9DG82
15	1201	43.1	543	2 Q6NUJ1
16	1099.5	39.4	525	2 Q8C1C1
17	786	28.2	449	2 Q8BJV5
18	772	27.7	402	2 Q8C1N0
19	552	19.8	953	2 Q9Y125
20	545	19.5	241	2 Q8N7T4
21	517	18.5	121	2 P79254
22	511	18.3	965	2 O15997
23	457	16.4	921	2 Q7PMW6
24	432.5	15.5	876	2 Q8IMH4
25	393	14.1	80	1 SAP_PIG
26	382	13.7	377	1 PSPB_MOUSE
27	379	13.6	376	1 PSPB_RAT
28	377	13.5	376	2 Q6IN44
29	349.5	12.5	378	2 Q35489
30	349.5	12.5	381	1 PSPB_HUMAN
31	343.5	12.3	458	2 Q95X02
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				Q61bq6 homo sapien
				P26779 b proactiva
				P10960 rattus norv
				Q6p7a4 rattus norv
				Q8bfq1 m mus muscu
				Q61207 mus muscu
				O13035 gallus gall
				Q78y70 xenopus lae
				Q642s6 xenopus lae
				Q8uvz4 brachydanio
				Q6ph48 brachydanio
				Q6p3g7 brachydanio
				Q9dg82 brachydanio
				Q6nuj1 homo sapien
				Q8c1c1 mus muscu
				Q8bjv5 mus muscu
				Q8c1n0 mus muscu
				Q9y125 drosophila
				Q8n7t4 homo sapien
				P79254 ovis aries
				O15997 bombyx mori
				Q7pmw6 anopheles g
				Q8imh4 drosophila
				P81405 sus scrofa
				P50405 mus muscu
				P22355 rattus norv
				Q6in44 rattus norv
				Q35489 cavia porce
				P07988 homo sapien
				Q95x02 naegleria f

ALIGNMENTS

Q9bkml naegleria f
Q9cu81 ovis aries
Q9u9p3 drosophila
Q7pj7 anopheles g
P17129 canis fami
P15285 oryctolagus
P79333 oryctolagus
Q9bkml naegleria f
Q94472 dictyosteli
Q6tyd9 trichinella
Q86pa4 drosophila
Q98ct5 arabidopsis
Q91zw6 arabidopsis
Q7pj6 anopheles g
Q9t05 ovis aries
Q75k05 dictyosteli
Q9as89 oryza sativ
Q18279 caenorhabd
Q9bd29 ovis aries
Q9m614 vitis ribar
Q9f77 nepenthes a
Q04057 cucurbita p
Q86ka8 dictyosteli
Q38934 arabidopsis
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Q39311 brassica na
Q9lux5 pyrus pyrif
Q8vy13 arabidopsis
Q41713 vigna ungui
Q816a9 theobroma c
Q8h0r9 cynara card
P42210 hordeum vul
Q94ia2 glycine max
Q9n275 ovis aries
P43072 brassica ol
Q9f78 nepenthes a
P42211 oryza sativ
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Q98ez1 helianthus
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Q9f79 nepenthes a
Q25430 lytechinus
Q61543 mus musculu
Q948p0 glycine max
Q2456 oryza sativ
Q39476 cynara card
Q688w6 oryza sativ
Q70bt3 physcomitre
Q816a8 theobroma c
Q9xec4 arabidopsis
Q9lgz3 oryza sativ
Q75x05 helicobacte
Q62638 rattus norv
Q92896 homo sapien
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Q94175 pneumocysti
Q98xu0 cicier ariet
Q75x61 helicobacte
Q75xj8 helicobacte
Q8c38 helicobacte
Q04593 arabidopsis

484 2 Q9BKML
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363 1 PSPB_CANFA
370 1 PSPB_RABIT
370 2 P79333
307 2 Q9BKML
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478 2 Q6RYD9
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316 2 Q86PA4
429 2 Q18276
213 2 Q9SCT5
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200 2 Q75K05
240 2 Q9AS89
402 2 Q18279
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174 2 Q9M614
507 2 Q9F77
513 1 ASFR_WUCPE
188 2 Q86KA8
486 2 Q38934
506 2 Q65390
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273 2 Q9LUX5
513 2 Q8VYL3
513 2 Q41713
514 2 Q8L6A9
107 2 Q8H0R9
508 1 ASFR_HORVU
514 2 Q94I22
205 2 Q9N275
292 2 Q43407
473 1 CYP1_CYNCA
514 2 Q9FRW8
496 1 ASFR_ORYSA
496 2 Q75L35
509 2 Q9S8Z1
509 2 Q96383
517 2 Q81654
514 2 Q9FRW9
909 2 Q25430
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509 2 Q39476
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495 2 Q9LGZ3
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1179 1 GLG1_HUMAN
1203 2 Q9P9D1
1160 2 GLG1_CRIGR
791 2 Q94175
204 2 Q98XU0
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1795 2 Q75XJ8
480 2 Q8C3E8
1927 2 Q04593
433 2 Q04593

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6.5 180
6.4 179.5
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4.8 134.5
4.8 134
4.8 134
4.8 133.5

RESULT 1
SAP_HUMAN
ID SAP_HUMAN STANDARD; PRT; 524 AA.
AC P07602; P07292; P15793; P78538; P78541; P78546; P78547; P78558;
AC Q92739; Q92740; Q92741; Q92742;
DT 01-APR-1998 (Rel. 07, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Proactivator polypeptide precursor [Contains: Saposin A (Protein A);
DE Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside
DE sulfate activator) (CSAct) (Dispersin) (Sulfatide/GM1 activator);
DE Saposin C (Co-beta-glucosidase) (Al activator) (Glucosylceramidase
DE activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D
DE (Protein C) (Component C)].
GN Name=PSAP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=90129043; PubMed=2515150;
RA Roxman E.G., Grabowski G.A.;
RT "Molecular cloning of a human co-beta-glucosidase cDNA: evidence that
RT four sphingolipid hydrolase activator proteins are encoded by single
RT genes in humans and rats.";
RL Genomics 5:486-492(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8925151; PubMed=2498298;
RA Nakano T., Sandhoff K., Stuenkel J., Christomanou H., Suzuki K.;
RT "Structure of full-length cDNA coding for sulfatide activator, a Co-
RT beta-glucosidase and two other homologous proteins: two alternate
RT forms of the sulfatide activator.";
RL J. Biochem. 105:152-154(1989).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM SAP-MU-0).
RC TISSUE=Brain, Eye, and Skin;
RX MEDLINE=23988257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 59-125 AND 304-513 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91192146; PubMed=2013321; DOI=10.1016/0014-5793(91)80308-P;
RA Holtschmidt H., Sandhoff K., Fuerst W., Kwon H.Y., Schnabel D.,
RA Suzuki K.;
RT "The organization of the gene for the human cerebroside sulfate
RT activator protein.";
RL FEBS Lett. 280:267-270(1991).
RN [5]
RP SEQUENCE OF 164-524 FROM N.A.
RX MEDLINE=88068647; PubMed=2825202;

RA Dewji N.N., Wenger D.A., O'Brien J.S.;
RT "Nucleotide sequence of cloned cDNA for human sphingolipid activator
RT protein 1 precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:8652-8656(1987).
RN [6]
RP PARTIAL SEQUENCE OF 60-142.
RX MEDLINE=89240739; PubMed=2717620;
RA Morimoto S., Martin B.M., Yamamoto Y., Kretz K.A., O'Brien J.S.,
RA Kishimoto Y.;
RT "Saposin A: second cerebroside activator protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:3389-3393(1989).
RN [7]
RP SEQUENCE OF 195-263 FROM N.A.
RX MEDLINE=86130593; PubMed=2868718;
RA Dewji N.N., Wenger D.A., Fujibayashi S., Donoviel M., Esch F.,
RA Hill F., O'Brien J.S.;
RT "Molecular cloning of the sphingolipid activator protein-1 (SAP-1),
RT the sulfatide sulfatase activator.";
RL Biochem. Biophys. Res. Commun. 134:989-994(1986).
RN [8]
RP SEQUENCE OF 195-274.
RC TISSUE=Kidney;
RX MEDLINE=91006165; PubMed=2209618;
RA Furst W., Schubert J., Machleidt W., Meyer H.E., Sandhoff K.;
RT "The complete amino-acid sequences of human ganglioside GM2 activator
RT protein and cerebroside sulfate activator protein.";
RL Eur. J. Biochem. 192:709-714(1990).
RN [9]
RP SEQUENCE OF 195-274.
RX MEDLINE=89207118; PubMed=3242555;
RA Kleinschmidt T., Christomanou H., Braunitzer G.;
RT "Complete amino-acid sequence of the naturally occurring A2 activator
RT protein for enzymic sphingomyelin degradation: identity to the
RT sulfatide activator protein (SAP-1).";
RL Biol. Chem. Hoppe-Seyler 369:1361-1365(1988).
RN [10]
RP SEQUENCE OF 311-390.
RX MEDLINE=88163077; PubMed=3442600;
RA Kleinschmidt T., Christomanou H., Braunitzer G.;
RT "Complete amino-acid sequence and carbohydrate content of the
RT naturally occurring glucosylceramide activator protein (Al activator)
RT absent from a new human Gaucher disease variant.";
RL Biol. Chem. Hoppe-Seyler 368:1571-1578(1987).
RN [11]
RP SEQUENCE OF 407-484.
RX MEDLINE=89000190; PubMed=3048308;
RA Furst W., Machleidt W., Sandhoff K.;
RT "The precursor of sulfatide activator protein is processed to three
RT different proteins.";
RL Biol. Chem. Hoppe-Seyler 369:317-328(1988).
RN [12]
RP PARTIAL SEQUENCE OF 405-484.
RX MEDLINE=89025876; PubMed=2845979;
RA Morimoto S., Martin B.M., Kishimoto Y., O'Brien J.S.;
RT "Saposin D: a sphingomyelinase activator.";
RL Biochem. Biophys. Res. Commun. 156:403-410(1988).
RN [13]
RP SEQUENCE OF 17-26.
RC TISSUE=Milk;
RX MEDLINE=92068206; PubMed=1958198;
RA Kondoh K., Hineno T., Sano A., Kakimoto Y.;
RT "Isolation and characterization of prosaposin from human milk.";
RL Biochem. Biophys. Res. Commun. 181:286-292(1991).
RN [14]
RP PARTIAL SEQUENCE (SAPOSIN B), AND STRUCTURE OF CARBOHYDRATES.
RC TISSUE=Urine;
RX MEDLINE=20032116; PubMed=10562467; DOI=10.1006/mgme.1999.2900;
RA Fluharty A.L., Lombardo C., Louis A., Stevens R.L., Whitelegge J.P.,
RA Waring A.J., To T., Fluharty C.B., Faull K.F.;
RT "Preparation of the cerebroside sulfate activator (CSAct or saposin B)
RT from human urine.";
RL Mol. Genet. Metab. 68:391-403(1999).
RN [15]

RP STRUCTURE OF CARBOHYDRATE ON ASN-215.
 RX MEDLINE=21110404; PubMed=11180632;
 RA Faull K.F., Johnson J., Kim M.J., To T., Whitelegge J.P.,
 RA Stevens R.L., Fluharty C.B., Fluharty A.L.;
 RT "Structure of the asparagine-linked sugar chains of porcine kidney and
 RT human urine cerebroside sulfate activator protein.";
 RL J. Mass Spectrom. 35:1416-1424(2000).
 RN [16]
 RN SAPOSIN D DISULFIDE BONDS.
 RP MEDLINE=99337688; PubMed=10406958;
 RA Tatti M., Salvioli R., Ciaffoni F., Pucci P., Andolfo A.,
 RA Amoresano A., Vaccaro A.M.;
 RT "Structural and membrane-binding properties of saposin D.";
 RL Eur. J. Biochem. 263:486-494(1999).
 RN [17]
 RN SAPOSIN B DISULFIDE BONDS.
 RP MEDLINE=2238398; PubMed=12510003; DOI=10.1016/S1046-5928(02)00597-1;
 RA Ahn V.E., Faull K.F., Whitelegge J.P., Higginson J., Fluharty A.L.,
 RA Prive G.G.;
 RT "Expression, purification, crystallization, and preliminary X-ray
 RT analysis of recombinant human saposin B.";
 RL Protein Expr. Purif. 27:186-193(2003).
 RN [18]
 RN MASS SPECTROMETRY.
 RP TISSUE-Urine;
 RX MEDLINE=99441404; PubMed=10510427;
 RA Faull K.F., Whitelegge J.P., Higginson J., To T., Johnson J.,
 RA Krutchinsky A.N., Standing K.G., Waring A.J., Stevens R.L.,
 RA Fluharty C.B., Fluharty A.L.;
 RT "Cerebroside sulfate activator protein (Saposin B): chromatographic
 RT and electrospray mass spectrometric properties.";
 RL J. Mass Spectrom. 34:1040-1054(1999).
 RN [19]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 195-273, AND MUTAGENESIS OF
 RP ILE-240.
 RX MEDLINE=2406333; PubMed=12518053; DOI=10.1073/pnas.0136947100;
 RA Ahn V.E., Faull K.F., Whitelegge J.P., Fluharty A.L., Prive G.G.;
 RT "Crystal structure of saposin B reveals a dimeric shell for lipid
 RT binding.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:38-43(2003).
 RN [20]
 RN REVIEW ON MLD VARIANTS.
 RP MEDLINE=95170731; PubMed=7866401;
 RA Gieselmann V., Zlotogora J., Harris A., Wenger D.A., Morris C.P.;
 RT "Molecular genetics of metachromatic leukodystrophy.";
 RL Hum. Mutat. 4:233-242(1994).
 RN [21]
 RN VARIANT MLD ILE-217.
 RX MEDLINE=90147748; PubMed=2302219;
 RA Rafi M.A., Zhang X.-L., Degala G., Wenger D.A.;
 RT "Detection of a point mutation in sphingolipid activator protein-1
 RT mRNA in patients with a variant form of metachromatic
 RT leukodystrophy.";
 RL Biochem. Biophys. Res. Commun. 166:1017-1023(1990).
 RN [22]
 RN SEQUENCE FROM N.A., AND VARIANT MLD ILE-217.
 RP MEDLINE=90207231; PubMed=2320574;
 RX

Query Match 100.0%; Score 2789; DB 1; Length 524;
 Best Local Similarity 100.0%; Pred. No. 3.5e-171;
 Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWPKPTVKS 60
 Db 1 MYALFLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWPKPTVKS 60

QY 61 LPCDICKDVTAAAGMLKDNATEEILVYLEKTCDWLPKPNMSACKEIVDSYLPVILDI 120
 Db 61 LPCDICKDVTAAAGMLKDNATEEILVYLEKTCDWLPKPNMSACKEIVDSYLPVILDI 120

QY 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVPFMANIPLLLY 180
 Db 121 IKGMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVPFMANIPLLLY 180

QY 181 PDGPRSKPQKNDGVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
 Db 181 PDGPRSKPQKNDGVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240

QY 241 CKNYISQYSEIAIOMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
 Db 241 CKNYISQYSEIAIOMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300

QY 301 PIKKHEVPAKSDVYCEVCEFLVKEVTCLIENNKTEKETLDAFDKMCCKLPSLSSECOEV 360
 Db 301 PIKKHEVPAKSDVYCEVCEFLVKEVTCLIENNKTEKETLDAFDKMCCKLPSLSSECOEV 360

QY 361 VDTYSSSILSLLEVSPELVCSMLHLCGSTRLPALTVHVTQPKDGGFCVCKKLGVYLD 420
 Db 361 VDTYSSSILSLLEVSPELVCSMLHLCGSTRLPALTVHVTQPKDGGFCVCKKLGVYLD 420

QY 421 RNLEKNSFKOILAALEKGCSPDPYQKQCDQFVAEYEPVLIETLVEMDPSFVCLKIG 480
 Db 421 RNLEKNSFKOILAALEKGCSPDPYQKQCDQFVAEYEPVLIETLVEMDPSFVCLKIG 480

QY 481 ACPQSAHKPLLGTCKICWGPSYWCQNTETAAQCNVAEHCKRHWN 524
 Db 481 ACPQSAHKPLLGTCKICWGPSYWCQNTETAAQCNVAEHCKRHWN 524

RESULT 2
 Q6IBQ6 PRELIMINARY; PRT; 524 AA.
 AC Q6IBQ6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE PSAP protein.
 GN Name=PSAP;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR456746; CAG33027.1; -
 DR GO; GO:0005764; C:lysosome; IEA.
 DR GO; GO:0006629; P:lipid metabolism; IEA.
 DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
 DR InterPro; IPR003119; Sapa.
 DR InterPro; IPR007856; Sapa_1.
 DR InterPro; IPR008138; Sapa_2.
 DR InterPro; IPR008140; Sapa_sub.
 DR InterPro; IPR008373; Saposin.
 DR InterPro; IPR008139; SaposinB.
 DR InterPro; IPR011001; Saposin_like.
 DR Pfam; PF02199; Sapa; 2.
 DR Pfam; PF05184; Sapa_1; 4.
 DR Pfam; PF03489; Sapa_2; 4.
 DR PRINTS; PR01797; SAPOSIN.
 DR ProDom; PD001732; Sapa_sub; 2.
 DR SMART; SM00162; SAPA; 2.
 SQ SEQUENCE 524 AA; 58096 MW; 71863A62484B94EF CRC64;

Query Match 99.7%; Score 2782; DB 2; Length 524;
 Best Local Similarity 99.8%; Pred. No. 9.9e-171;
 Matches 523; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYALFLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWPKPTVKS 60
 Db 1 MYALFLASLLGAALAGPVLGKECTRGSAVWCNQVKTASDCGAVKHCLQTVWPKPTVKS 60

QY 61 LPCDICKDVTAAAGMLKDNATEEILVYLEKTCDWLPKPNMSACKEIVDSYLPVILDI 120
 Db 61 LPCDICKDVTAAAGMLKDNATEEILVYLEKTCDWLPKPNMSACKEIVDSYLPVILDI 120

QY 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLY 180
 D5 121 IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLY 180
 QY 181 PDGPRSKPQKNGDVCDQCIQWYTDIQTAVRTNSTFVQALVEHVKEECDRLGPMADI 240
 D5 181 PDGPRSKPQKNGDVCDQCIQWYTDIQTAVRTNSTFVQALVEHVKEECDRLGPMADI 240
 QY 241 CKNYISQYSEITAIQMMHMQKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
 D5 241 CKNYISQYSEITAIQMMHMQKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
 QY 301 PIKHEVPAKGDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMKCSKLPKSLSECEQEV 360
 D5 301 PIKHEVPAKGDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMKCSKLPKSLSECEQEV 360
 QY 361 VDTYSSILSLILEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVCKKLGVYLD 420
 D5 361 VDTYSSILSLILEEVSPELVCSMLHLCSGTRLPALTVHVTQPKDGGFCEVCKKLGVYLD 420
 QY 421 RNLEKNSTKQILAALEKGCFLPDYQKQCDQFVAEYEPVLIETLVEMDPSFVCLKIG 480
 D5 421 RNLEKNSTKQILAALEKGCFLPDYQKQCDQFVAEYEPVLIETLVEMDPSFVCLKIG 480
 QY 481 ACPSAHKPLLGTEKIMGSPSYWCQNTETAACNAVEHCKRHVN 524
 D5 481 ACPSAHKPLLGTEKIMGSPSYWCQNTETAACNAVEHCKRHVN 524

RESULT 3

SAP_BOVIN
 ID SAP_BOVIN STANDARD; PRT; 525 AA.
 AC P26779; QN264;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Proactivator polypeptide precursor [Contains: Saposin A (protein A);
 DE Saposin B (sphingolipid activator protein 1) (SAP-1) (cerebroside
 DE sulfate activator) (CSact) (Dispersin) (Sulfatide/GM1 activator);
 DE Saposin C (Co-beta-glucosidase) (AI activator) (Glucosylceramidase
 DE activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D
 DE (Protein C) (Component C)].
 GN Name=PSAP;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANTS.
 RC TISSUE=Mammary gland;
 RA Azuma N., Yoshida K.;
 RT "RT-PCR cloning of bovine prosaposin.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 312-391.
 RC TISSUE=Spleen;
 RX MEDLINE=92207994; PubMed=1554743; DOI=10.1016/0167-4838(92)90426-E;
 RA Sano A., Mizuno T., Kondoh K., Hineno T., Ueno S.-I., Kakimoto Y.,
 RA Morita N.;
 RT "Saposin-C from bovine spleen; complete amino acid sequence and
 RT relation between the structure and its biological activity.";
 RL Biochim. Biophys. Acta 1120:75-80(1992).
 CC -!- FUNCTION: The lysosomal degradation of sphingolipids takes place
 CC by the sequential action of specific hydrolases. Some of these
 CC enzymes require specific low-molecular mass, non-enzymic proteins:
 CC the sphingolipids activator proteins (coproteins) (By similarity).
 CC -!- FUNCTION: Saposin A and saposin C stimulate the hydrolysis of
 CC glucosylceramide by beta-glucosylceramidase (EC 3.2.1.45) and
 CC galactosylceramide by beta-galactosylceramidase (EC 3.2.1.46).
 CC Saposin C apparently acts by combining with the enzyme and acidic
 CC lipid to form an activated complex, rather than by solubilizing

the substrate.
 -!- FUNCTION: Saposin B stimulates the hydrolysis of galacto-
 CC cerebroside sulfate by arylsulfatase A (EC 3.1.6.8), GM1
 CC gangliosides by beta-galactosidase (EC 3.2.1.23) and
 CC globotriaosylceramide by alpha-galactosidase A (EC 3.2.1.22).
 CC Saposin B forms a solubilizing complex with the substrates of the
 CC sphingolipid hydrolases (By similarity).
 CC -!- FUNCTION: Saposin D is a specific sphingomyelin phosphodiesterase
 CC activator (EC 3.1.4.12) (By similarity).
 CC -!- SUBUNIT: Saposin B is a homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Lysosomal.
 CC -!- PTM: This precursor is proteolytically processed to 4 small
 CC peptides, which are similar to each other and are sphingolipid
 CC hydrolase activator proteins (By similarity).
 CC -!- SIMILARITY: Contains 2 saposin A-type domains.
 CC -!- SIMILARITY: Contains 2 saposin B-type domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)
 CC or send an email to license@sib-sib.ch.
 CC -----
 CC EMBL; AB036791; BAA95677.1; -.
 CC HSSP; Q92739; 1M12.
 CC InterPro; IPR003119; Sapa.
 CC InterPro; IPR007856; SapB_1.
 CC InterPro; IPR008138; SapB_2.
 CC InterPro; IPR008140; SapB_sub.
 CC InterPro; IPR008373; Saposin.
 CC InterPro; IPR011001; Saposin like.
 CC InterPro; IPR008139; SaposinB.
 CC Pfam; PF02199; Sapa; 2.
 CC Pfam; PF05184; SapB_1; 4.
 CC Pfam; PF03489; SapB_2; 4.
 CC PRINTS; PR01797; SAPOSIN.
 CC ProDom; PD01732; SapB_sub; 2.
 CC ProDom; PD008002; Surfactant_B; 1.
 CC SMART; SM00162; SAPA; 2.
 CC SMART; SM00741; SapB; 4.
 CC Direct protein sequencing; Glycoprotein; Lysosome; Repeat; Signal;
 CC Sphingolipid metabolism.
 CC SIGNAL 1 16 Potential.
 CC PROPEP 17 58
 CC CHAIN 60 142 Saposin A.
 CC PROPEP 144 195
 CC CHAIN 196 275 Saposin B.
 CC PROPEP 277 310
 CC CHAIN 312 392 Saposin C.
 CC PROPEP 393 404
 CC CHAIN 406 487 Saposin D.
 CC PROPEP 489 525
 CC DOMAIN 21 54
 CC DOMAIN 59 142 Saposin-like type A 1.
 CC DOMAIN 194 276 Saposin-like type B 1.
 CC DOMAIN 312 393 Saposin-like type B 2.
 CC DOMAIN 406 487 Saposin-like type B 3.
 CC DOMAIN 492 525 Saposin-like type B 4.
 CC DISULFID 63 138 By similarity.
 CC DISULFID 66 132 By similarity.
 CC DISULFID 94 106 By similarity.
 CC DISULFID 199 272 By similarity.
 CC DISULFID 202 266 By similarity.
 CC DISULFID 231 242 By similarity.
 CC DISULFID 316 389 By similarity.
 CC DISULFID 319 383 By similarity.
 CC DISULFID 347 358 By similarity.
 CC DISULFID 410 483 By similarity.
 CC DISULFID 413 477 By similarity.
 CC DISULFID 441 452 By similarity.
 CC CARBOHYD 80 N-linked (GlcNAc. .) (Potential).
 CC 80

FT CARBOHYD 101 101 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 216 216 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 333 333 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 427 427 N-linked (GlcNAc...) (Potential).
 FT VARIANT 127 127 H -> R.
 FT VARIANT 260 263 MOPK -> IRIR.
 FT CONFLICT 317 317 E -> Q (in Ref. 2).
 FT CONFLICT 367 367 R -> S (in Ref. 1).
 SQ SEQUENCE 525 AA; 58120 MW; 293AF0CFB9C4FA99 CRC64;

Query Match 87.0%; Score 2425.5; DB 1; Length 525;
 Best Local Similarity 84.2%; Pred No 8.5e-148;
 Matches 442; Conservative 45; Mismatches 37; Indels 1; Gaps 1;

QY 1 MYALFLLASLLGAALAGPVILGKECTRGSAVQCNVKTASDCGAVGKCLQTVNNKPTVKS 60
 DB 1 MYSFVFLASLLGALLASPVILGRECTRGSAVQCNVKTAAADCGAVQHCLQTVWSKPTVKS 60

QY 61 LECDDICKDVVTAAGDMLKDNATEEELVLEKTCDWLPKPNMSACKKEIVDSYLVILDM 120
 DB 61 LECDDICKDVITAGNLLKDNATEEELVLEKTCDWLPKPNMSACKKEIVDSYLVILDM 120

QY 121 IKGMSRPEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVWVAFMANIPLLLY 180
 DB 121 IKGQSHPEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVWVAFMANIPLFLY 180

QY 181 PDGPRSRPQPKD-NGDVQCDCIQMVTDIQTAVRTNSTFVQALVEHVEECEDRLGFGMAD 239
 DB 181 PDGSHSRPQPKANGNVQCDCIQLVTDVQEARLNTSTFVEALVDHAKKECDRLGFGMSD 240

QY 240 ICKNYSIQSEYAIQMMHMQKEICALVGFCDCEKEMPMQTLVPAKVASKQVIFALELIV 299
 DB 241 MCKNYINQYSEYAIQMMHMQKEICVLAGFCDEKEMPMKTLVPAEVVSENVIPALGLV 300

QY 300 EPIKKEHVPKSDVCEVCEFLVKEVTKLIDNNKTEKELIDAFDKMCKLPSLSEECQE 359
 DB 301 EPIKDPAPAKADIYCEVCEFLVKEVTKLIDNNRTEELHDLKVCSLFTSLAEQCE 360

QY 360 VVDYTGSSILSLLEBVSPELVCSMLHLCSTGTRLPALTVHVTQPKDGGFCEYCKKLVGL 419
 DB 361 VVDYTGSRSLSLLEASPELVCSMLHLCSSRGLPAATVRVMPKDGDFCEYCKKLVGL 420

QY 420 DRNLEKNTKQRIILAEKGSFLPDPYQKQDQFVAEYEPVLIILVEVMDPSFVCLKI 479
 DB 421 DRNLEKNTKQRIILAEKGSFLPDPYQKQDQFVTEYEPVLIILVEVMDPSFVCLKI 480

QY 480 GACPSAHPKLLCTEKCIMGSPSYWQNTETAAOCNAVEHCKRHVN 524
 DB 481 GACPAHKKPLLAGKCKVWGSPSYWQNMESALCNAVEHCKRHVN 525

RESULT 4

SAP_RAT STANDARD; PRT; 554 AA.
 ID P10360; Q62841; Q64190;
 AC 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sulfated glycoprotein 1 precursor (SGP-1) (Prosaposin).
 GN Name=Peap; Synonyms=Sppl;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Sertoli cells;
 RX MEDLINE=89000647; PubMed=3048385;
 RA Collard M.W., Sylvester S.R., Tsuruta J.K., Griswold M.D.;
 RT "Biosynthesis and molecular cloning of sulfated glycoprotein 1
 RT secreted by rat Sertoli cells: sequence similarity with the 70-
 RT kilodalton precursor to sulfatide/GM1 activator.";
 RL Biochemistry 27:4557-4564 (1988).

RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Sertoli;
 RX MEDLINE=96128541; PubMed=8573994;
 RA Morales C.R., El-Alfy M., Zhao Q., Igdoura S.A.;
 RT "Molecular role of sulfated glycoprotein-1 (SGP-1/prosaposin) in
 RT Sertoli cells.";
 RL Histol. Histopathol. 10:1023-1034 (1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testicle;
 RX MEDLINE=96175245; PubMed=8601692;
 RA Morales C.R., El-Alfy M., Zhao Q., Igdoura S.A.;
 RT "Expression and tissue distribution of rat sulfated glycoprotein-1
 RT (prosaposin).";
 RL J. Histochem. Cytochem. 44:327-337 (1996).
 CC -|- SURCELLULAR LOCATION: Extracellular.
 CC -|- SIMILARITY: Contains 2 saposin A-type domains.
 CC -|- SIMILARITY: Contains 4 saposin B-type domains.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M19936; AAA42136.1; -;
 CC EMBL; S81353; AAB36042.2; -;
 CC EMBL; S81373; AAB36233.2; -;
 CC PIR; A28716; A28716.
 CC HSSP; Q92739; IN69.
 CC RGD; 3423; Peap.
 CC InterPro; IPR003119; Sapa.
 CC InterPro; IPR007856; Sapp_1.
 CC InterPro; IPR008138; Sapp_2.
 CC InterPro; IPR008140; Sapp_sub.
 CC InterPro; IPR008373; Saposin.
 CC InterPro; IPR011001; Saposin like.
 CC InterPro; IPR008139; SaposinB.
 CC Pfam; PF02199; Sapa; 2.
 CC Pfam; PF05184; Sapp_1; 3.
 CC Pfam; PF03489; Sapp_2; 4.
 CC PRINTS; PR01797; SAPOSIN.
 CC ProDom; PD001732; Sapp_sub; 1.
 CC Direct protein sequencing; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 554 Sulfated glycoprotein 1.
 FT DOMAIN 21 54 Saposin-like type A 1.
 FT DOMAIN 61 138 Saposin-like type B 1.
 FT DOMAIN 193 274 Saposin-like type B 2.
 FT DOMAIN 310 391 Saposin-like type B 3.
 FT DOMAIN 435 516 Saposin-like type B 4.
 FT DOMAIN 521 554 Saposin-like type A 2.
 FT DISULFID 63 138 By similarity.
 FT DISULFID 66 132 By similarity.
 FT DISULFID 94 106 By similarity.
 FT DISULFID 197 270 By similarity.
 FT DISULFID 200 264 By similarity.
 FT DISULFID 229 240 By similarity.
 FT DISULFID 314 387 By similarity.
 FT DISULFID 317 381 By similarity.
 FT DISULFID 345 356 By similarity.
 FT DISULFID 439 512 By similarity.
 FT DISULFID 442 506 By similarity.
 FT DISULFID 470 481 By similarity.
 FT CARBOHYD 80 80 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 214 214 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 331 331 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 456 456 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 115 115 P -> L (in Ref. 2 and 3).
 FT CONFLICT 299 299 D -> E (in Ref. 2).

```
FT CONFLICT 462 462 I -> V (in Ref. 3)
FT CONFLICT 527 527 W -> R (in Ref. 3)
FT CONFLICT 536 536 S -> M (in Ref. 3)
SQ SEQUENCE 554 AA; 61123 MW; DFE3FA3A0520C6B CRC64;

Query Match 71.6%; Score 1996; DB 1; Length 554;
Best Local Similarity 66.3%; Pred. No. 3.8e-120;
Matches 368; Conservative 77; Mismatches 78; Indels 32; Gaps 3;

QY 1 MYALLASLIGALAGPVLGLKETRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
Db 1 MYALLASLIGALAGPVLGLKETRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
QY 61 LPCDICKVTVTAAGDMLKDNATEBEILVYLEKTCWLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKVTVTAAGDMLKDNATEBEILVYLEKTCWLPKPNMSASCKEIVDSYLPVILDI 120
QY 121 IKGMSRPFGEVCSALNLCESLOKHLAEINHOQLESNKIPELDMTEVVVAPPMANIPLLLY 180
Db 121 IKGMSRPFGEVCSALNLCESLOKHLAEINHOQLESNKIPELDMTEVVVAPPMANIPLLLY 180
QY 181 PQDGRSKPOPKNGDVCDQCIQMTVDIQTAVRTNSTFVQALVEHVKCECDRLGPGVADI 240
Db 181 PQDGRSKPOPKNGDVCDQCIQMTVDIQTAVRTNSTFVQALVEHVKCECDRLGPGVADI 240
QY 180 PQDRSPQPKANEDVCDQCMKLVTDIQTAVRTNSSFVQGLVDHVKEDCDRLGPGVSDI 239
Db 180 PQDRSPQPKANEDVCDQCMKLVTDIQTAVRTNSSFVQGLVDHVKEDCDRLGPGVSDI 239
QY 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDCEKMPQTLVPAKVASKNVIPALELVE 300
Db 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDCEKMPQTLVPAKVASKNVIPALELVE 300
QY 240 CKNYVDQYSEVAVQMMHMQPKEICVMVGFCDCEKMPQTLVPAKAIKILPALELTD 299
Db 240 CKNYVDQYSEVAVQMMHMQPKEICVMVGFCDCEKMPQTLVPAKAIKILPALELTD 299
QY 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELDAFDKMSCKLPSLSECOEV 360
Db 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELDAFDKMSCKLPSLSECOEV 360
QY 300 PVEQDVIQANQVIFCQVQVLMVRLSELIINNAATELLIKGLSKACSLPAPASTKCOEV 359
Db 300 PVEQDVIQANQVIFCQVQVLMVRLSELIINNAATELLIKGLSKACSLPAPASTKCOEV 359
QY 361 VDTYSSILSILLEVSPVCSLMHLCSG-----TRLP----- 394
Db 361 VDTYSSILSILLEVSPVCSLMHLCSG-----TRLP----- 394
QY 360 LVTFGPSLLDVLMEHVNPNFLCGVISLCSANPNLVGTLQEPAAAIVSALPKPEAPPKQPE 419
Db 360 LVTFGPSLLDVLMEHVNPNFLCGVISLCSANPNLVGTLQEPAAAIVSALPKPEAPPKQPE 419
QY 395 -----ALTVHTQPTQKGGFCEVCKLVGLYDRNLEKNTKOBILAALEKGCSEFLPDYQK 449
Db 395 -----ALTVHTQPTQKGGFCEVCKLVGLYDRNLEKNTKOBILAALEKGCSEFLPDYQK 449
QY 420 EPKQALRAHVPPQKNGFCEVCKLVLYLEHLEKNTKOBILAALEKGCSEFLPDYQK 479
Db 420 EPKQALRAHVPPQKNGFCEVCKLVLYLEHLEKNTKOBILAALEKGCSEFLPDYQK 479
QY 450 QCDQFVARYEPVLBILEVMDPSFVCLIKIGACPSAHKPLLGTEKICWPGSYWQNTFTA 509
Db 450 QCDQFVARYEPVLBILEVMDPSFVCLIKIGACPSAHKPLLGTEKICWPGSYWQNTFTA 509
QY 480 QCDEFVARYEPVLBILEVMDPSFVCSKIGVCPKAYKLLGTEKICWPGSYWQNTFTA 539
Db 480 QCDEFVARYEPVLBILEVMDPSFVCSKIGVCPKAYKLLGTEKICWPGSYWQNTFTA 539
QY 510 AQCNVAHECKRHVN 524
Db 510 AQCNVAHECKRHVN 524
QY 540 ARCNVAHECKRHVN 554
Db 540 ARCNVAHECKRHVN 554

RESULT 5
Q6P7A4 PRELIMINARY; PRT; 553 AA.
AC Q6P7A4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Proapsosin.
GN Name=Psap;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallus D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC061759; AAH61759.1; -.
DR GO; GO:0005764; C:lysosome; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
DR InterPro; IPR003119; SApA.
DR InterPro; IPR007856; SapB_1.
DR InterPro; IPR008138; SapB_2.
DR InterPro; IPR008140; SapB_sub.
DR InterPro; IPR008373; Saposin.
DR InterPro; IPR008139; SaposinB.
DR InterPro; IPR011001; Saposin_like.
DR Pfam; PF02199; SApA; 2.
DR Pfam; PF05184; SapB_1; 3.
DR Pfam; PF03489; SapB_2; 4.
DR PRINTS; PR01797; SAPOSIN.
DR ProDom; PD001732; SapB_sub; 1.
DR SMART; SM00162; SApA; 2.
SQ SEQUENCE 553 AA; 61039 MW; 63F3DD5E0C523393 CRC64;

Query Match 71.1%; Score 1982.5; DB 2; Length 553;
Best Local Similarity 66.3%; Pred. No. 2.8e-119;
Matches 368; Conservative 75; Mismatches 79; Indels 33; Gaps 4;

QY 1 MYALLASLIGALAGPVLGLKETRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
Db 1 MYALLASLIGALAGPVLGLKETRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
QY 61 LPCDICKVTVTAAGDMLKDNATEBEILVYLEKTCWLPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPCDICKVTVTAAGDMLKDNATEBEILVYLEKTCWLPKPNMSASCKEIVDSYLPVILDI 120
QY 121 IKGMSRPFGEVCSALNLCESLOKHLAEINHOQLESNKIPELDMTEVVVAPPMANIPLLLY 180
Db 121 IKGMSRPFGEVCSALNLCESLOKHLAEINHOQLESNKIPELDMTEVVVAPPMANIPLLLY 180
QY 181 PQDGRSKPOPKNGDVCDQCIQMTVDIQTAVRTNSTFVQALVEHVKCECDRLGPGVADI 240
Db 181 PQDGRSKPOPKNGDVCDQCIQMTVDIQTAVRTNSTFVQALVEHVKCECDRLGPGVADI 240
QY 180 PQDRSPQPKANEDVCDQCMKLVTDIQTAVRTNSSFVQGLVDHVKEDCDRLGPGVSDI 239
Db 180 PQDRSPQPKANEDVCDQCMKLVTDIQTAVRTNSSFVQGLVDHVKEDCDRLGPGVSDI 239
QY 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDCEKMPQTLVPAKVASKNVIPALELVE 300
Db 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDCEKMPQTLVPAKVASKNVIPALELVE 300
QY 240 CKNYVDQYSEVAVQMMHMQPKEICVMVGFCDCEKMPQTLVPAKAIKILPALELTD 299
Db 240 CKNYVDQYSEVAVQMMHMQPKEICVMVGFCDCEKMPQTLVPAKAIKILPALELTD 299
QY 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELDAFDKMSCKLPSLSECOEV 360
Db 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELDAFDKMSCKLPSLSECOEV 360
QY 300 PVEQDVIQANQVIFCQVQVLMVRLSELIINNAATELLIKGLSKACSLPAPASTKCOEV 358
Db 300 PVEQDVIQANQVIFCQVQVLMVRLSELIINNAATELLIKGLSKACSLPAPASTKCOEV 358
QY 361 VDTYSSILSILLEVSPVCSLMHLCSG-----TRLP----- 394
Db 361 VDTYSSILSILLEVSPVCSLMHLCSG-----TRLP----- 394
QY 359 LVTFGPSLLDVLMEHVNPNFLCGVISLCSANPNLVGTLQEPAAAIVSALPKPEAPPKQPE 418
Db 359 LVTFGPSLLDVLMEHVNPNFLCGVISLCSANPNLVGTLQEPAAAIVSALPKPEAPPKQPE 418
QY 395 -----ALTVHTQPTQKGGFCEVCKLVLYLEHLEKNTKOBILAALEKGCSEFLPDYQK 449
Db 395 -----ALTVHTQPTQKGGFCEVCKLVLYLEHLEKNTKOBILAALEKGCSEFLPDYQK 449
QY 419 EPKQALRAHVPPQKNGFCEVCKLVLYLEHLEKNTKOBILAALEKGCSEFLPDYQK 478
Db 419 EPKQALRAHVPPQKNGFCEVCKLVLYLEHLEKNTKOBILAALEKGCSEFLPDYQK 478
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Db 480 QCDDFVAEYEPLELLVEVMDPGVCSKIGVCSAYKLLIGTEKCVGPRSYQWQNMETA 539
 QY 510 AOCNAVECHKRVWN 524
 Db 540 ARCAVNDCHKRVWN 554

RESULT 7

SAP_MOUSE
 ID SAP_MOUSE STANDARD; PRT; 557 AA.
 AC Q61207; Q60861; Q64006; Q64219;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 05-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sulfated glycoprotein 1 precursor (SGP-1) (Prosaposin).
 GN Name=Peap; Synonymus=SGpl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92272718; PubMed=1590788;
 RA Tsuda M., Sakiyama T., Endo H., Kitagawa T.;
 RT "The primary structure of mouse saposin";
 RL Biochem. Biophys. Res. Commun. 184:1266-1272 (1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94272317; PubMed=8003952;
 RA Sprecher-Levy H., Orr-Urtreger A., Lonai P., Horowitz M.;
 RT "Murine prosaposin: expression in the reproductive system of a gene
 implicated in human genetic disease";
 RL Cell. Mol. Biol. 40:233-233 (1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96084310; PubMed=8565332;
 RA Cao Q.P., Crain W.R.;
 RT "Expression of SGP-1 mRNA in preimplantation mouse embryos";
 RL Dev. Genet. 17:263-271 (1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RA Zhao Q.Q., Hay N.N., Morales C.R.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- SIMILARITY: Contains 2 saposin A-type domains.
 CC -!- SIMILARITY: Contains 4 saposin B-type domains.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; S36200; AAB22175.1; -
 DR EMBL; S71616; AAB31059.1; -
 DR EMBL; U27340; AAA92567.1; -
 DR EMBL; U57999; AAB02695.1; -
 DR PIR; JH0604; JH0604.
 DR HSP; Q92739; 1N69.
 DR MGD; MGI:97783; Fsap.
 DR InterPro; IPR003119; Sapa.
 DR InterPro; IPR007856; SApB.1.
 DR InterPro; IPR008138; SApB.2.
 DR InterPro; IPR008140; SApB_sub.
 DR InterPro; IPR008373; Saposin.
 DR InterPro; IPR01001; Saposin-like.
 DR InterPro; IPR008139; SaposinB.
 DR Pfam; PF02199; Sapa; 2.

DR Pfam; PF05184; SapB.1; 4.
 DR Pfam; PF03489; SapB.2; 4.
 DR PRINTS; PR01797; SAPOSIN.
 DR ProDom; PD001732; SapB_sub; 1.
 KW Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 16 By similarity.
 FT CHAIN 17 557 Sulfated glycoprotein 1.
 FT DOMAIN 21 54 Saposin-like type A 1.
 FT DOMAIN 59 142 Saposin-like type B 1.
 FT DOMAIN 193 277 Saposin-like type B 2.
 FT DOMAIN 313 394 Saposin-like type B 3.
 FT DOMAIN 438 519 Saposin-like type B 4.
 FT DOMAIN 524 557 Saposin-like type A 2.
 FT DISULFID 63 138 By similarity.
 FT DISULFID 66 132 By similarity.
 FT DISULFID 94 106 By similarity.
 FT DISULFID 197 273 By similarity.
 FT DISULFID 200 267 By similarity.
 FT DISULFID 229 240 By similarity.
 FT DISULFID 317 390 By similarity.
 FT DISULFID 320 384 By similarity.
 FT DISULFID 348 359 By similarity.
 FT DISULFID 442 515 By similarity.
 FT DISULFID 445 509 By similarity.
 FT DISULFID 473 484 By similarity.
 FT CARBOHYD 80 80 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 214 214 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 459 459 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 83 83 Q -> E (in Ref. 2).
 FT CONFLICT 158 158 I -> V (in Ref. 3).
 FT CONFLICT 160 160 Missing (in Ref. 2).
 FT CONFLICT 171 172 MS -> SA (in Ref. 3).
 FT CONFLICT 244 244 V -> L (in Ref. 2).
 FT CONFLICT 254 254 M -> I (in Ref. 3).
 FT CONFLICT 255 255 L -> W (in Ref. 2).
 FT CONFLICT 260 262 Missing (in Ref. 3).
 FT CONFLICT 307 307 N -> D (in Ref. 2).
 FT CONFLICT 322 322 P -> L (in Ref. 2).
 FT CONFLICT 349 350 AL -> GV (in Ref. 1).
 FT CONFLICT 367 367 G -> D (in Ref. 3).
 FT CONFLICT 370 370 L -> Q (in Ref. 2).
 FT CONFLICT 373 373 I -> D (in Ref. 3).
 FT CONFLICT 391 391 A -> T (in Ref. 3).
 FT CONFLICT 393 393 R -> L (in Ref. 3).
 FT CONFLICT 406 406 A -> R (in Ref. 2 and 3).
 FT CONFLICT 430 430 P -> R (in Ref. 2).
 FT CONFLICT 445 445 C -> F (in Ref. 3).
 FT CONFLICT 448 448 L -> P (in Ref. 4).
 SQ SEQUENCE 557 AA; 61422 MW; 134593E20499E35E CRC64;
 Query Match 69.5%; Score 1938.5; DB 1; Length 557;
 Best Local Similarity 63.6%; Pred. No. 1.9e-116;
 Matches 355; Conservative 78; Mismatches 90; Indels 35; Gaps 3;
 Qy 1 MYALFLASLILGAALAGVLGLKECTRGSAVCONVKATSCGAVKHCLQVWVKPTVKS 60
 Db 1 MYALFASLLATALTSPVQDPKTCGSAVLCDVKTAVDGAVKHCCQWVSKPTAKS 60
 Qy 61 LPCDICKVDVTAAGDMLKDNATEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
 Db 61 LPCDICKTVVTEAGNLLKDNATQBEILHYLEKTCQWVHDSLSASCKEIVDSYLPVILDM 120
 Qy 121 IKGEMSRPGEVCSALNLCESLQKHLAEHLNKHQLESNKIPELDMTEVVAPFWANIPILLY 180
 Db 121 IKGEMSNPGEVCSALNLCQSLQELAEQN-QKLESNKIPEDVWVAPFWMSNIPILLY 179
 Qy 181 PQDGRPKPOPKDNGDVQCDCIQMVTDITQAVRTNSTFVQALVEHVEECEDRLGPGVADI 240
 Db 180 PQDHPRSQPOPKANEDVQCDCMKLVSDVQTAVKTNSSFIQGFVDHVKEDCDRLGPGVSDI 239
 Qy 241 CKNYISOYSEIAIQMMHM-----QPKETCALVGFCDEVKEMPMQTLVPAKASKVIPAILE 297
 Db 241 CKNYISOYSEIAIQMMHM-----QPKETCALVGFCDEVKEMPMQTLVPAKASKVIPAILE 297

Db 240 CKNYVDQYSEVCQMLMHMQDQPKXICVLACGFCNEKVPKMLVLPATETIKNLPAL 299
 QY 298 LVEPIKKEHVPKSDYCEVCEFLVKEVTKLIDNNKTEKILDAFDKWCCKLPKSLSEB 357
 Db 300 WMDPYEOLVQAHNVILQTCQFVNNKFSSELVNNATBELLVKGLSNACALLPDPARTKC 359
 QY 358 QBVVDYTGSSILSILLESVPELVCSMLHLCSG----- 390
 Db 360 QEVGTGFGSLDIIIFHVNPSLSCGVIGLCARPELVEALQAPATVSAALLKEPPTPK 419
 QY 391 -----TRLPALTVHTVQPKDGGFCVCKKLVGLYDRNLEKNSTKOBILAALEKGCFLPDP 446
 Db 420 QPAQPKQALPAHPVPPQKNGGFCVCKKLVLYLEHLEKNSTKOBILAALEKGCFLPDP 479
 QY 447 YQKQCDQFVAEYEPVLIILVEMDPSPFVCLKIGACPSAHKPLLTGTEKICWGPSWQNT 506
 Db 480 YQKQCDQFVAEYEPVLIILVEMDPSPFVCLKIGACPSAHKPLLTGTEKICWGPSWQNT 539
 QY 507 ETAAOCNAVEHCKRHVN 524
 Db 540 ETAAOCNAVDHCKRHVN 557

RESULT 8

SAP_CHICK STANDARD; PRT; 518 AA.
 ID SAP_CHICK
 AC O13035;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Proactivator polypeptide precursor [Contains: Saposin A; Saposin B;
 DE Saposin C; Saposin D].
 GN Name=PSAP;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_taxid=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 194-203.
 RC TISSUE=Brain, and Liver;
 RX MEDLINE=98129745; PubMed=9461526;
 RA Azuma N., Seo H.-C., Lie O., Fu Q., Gould R.M., Hiraiwa M., Burt D.W.,
 RA Paton I.R., Morrice D.R., O'Brien J.S., Kishimoto Y.;
 RT "Cloning, expression and map assignment of chicken prosaposin.";
 RL Biochem. J. 330:321-327(1998).
 RN [2]

SEQUENCE FROM N.A.
 RA Altman N., Horowitz M.;
 RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: The lysosomal degradation of sphingolipids takes place
 CC by the sequential action of specific hydrolases. Some of these
 CC enzymes require specific low-molecular mass, non-enzymic proteins:
 CC the sphingolipids activator proteins (coproteins) (By similarity).
 CC -!- FUNCTION: Saposin A and saposin C stimulate the hydrolysis of
 CC glucosylceramide by beta-glucosylceramidase (EC 3.2.1.45) and
 CC galactosylceramide by beta-galactosylceramidase (EC 3.2.1.46).
 CC Saposin C apparently acts by combining with the enzyme and acidic
 CC lipid to form an activated complex, rather than by solubilizing
 CC the substrate (By similarity).
 CC -!- FUNCTION: Saposin B stimulates the hydrolysis of galacto-
 CC cerebroside sulfate by arylsulfatase A (EC 3.1.6.8) and
 CC gangliosides by beta-galactosidase (EC 3.2.1.23) and
 CC globotriaosylceramide by alpha-galactosidase A (EC 3.2.1.22).
 CC Saposin B forms a solubilizing complex with the substrates of the
 CC sphingolipid hydrolases (By similarity).
 CC -!- FUNCTION: Saposin D is a specific sphingomyelin phosphodiesterase
 CC activator (EC 3.1.4.12) (By similarity).
 CC -!- SUBUNIT: Saposin B is a homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).
 CC -!- PTM: This precursor is proteolytically processed to 4 small
 CC peptides, which are similar to each other and are sphingolipid
 CC hydrolase activator proteins (By similarity).

CC -!- SIMILARITY: Contains 2 saposin A-type domains.
 CC -!- SIMILARITY: Contains 4 saposin B-type domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB003471; BAA19914.1; -;
 DR EMBL; AF108656; AAF05899.1; -;
 DR HSPF; Q92739; IN69.
 DR InterPro; IPR003119; Sapa.
 DR InterPro; IPR007856; SapaB.1.
 DR InterPro; IPR008138; SapaB.2.
 DR InterPro; IPR008140; SapaB_sub.
 DR InterPro; IPR008373; Saposin.
 DR InterPro; IPR011001; Saposin_like.
 DR InterPro; IPR008139; SaposinB.
 DR Pfam; PF02199; Sapa; 2.
 DR Pfam; PF05184; SapaB.1; 4.
 DR Pfam; PF03489; SapaB.2; 4.
 DR PRINTS; PR01797; SAFOSIN.
 DR PRODOM; PD001732; SapaB_sub; 1.
 DR SMART; SM00162; SAPA; 2.
 DR SMART; SM00741; Sapa; 4.
 KW Direct protein sequencing; Glycoprotein; GM2-gangliosidosis; Lysosome;
 KW Repeat; Signal; Sphingolipid metabolism.
 FT SIGNAL; 1 17 Potential.
 FT PROPEP; 18 60
 FT CHAIN; 61 143 Saposin A.
 FT PROPEP; 145 193
 FT CHAIN; 194 276 Saposin B.
 FT PROPEP; 278 305
 FT CHAIN; 307 387 Saposin C.
 FT PROPEP; 389 398
 FT CHAIN; 399 480 Saposin D.
 FT PROPEP; 482 518
 FT DOMAIN; 22 55 Saposin-like type A.1.
 FT DOMAIN; 60 143 Saposin-like type B.1.
 FT DOMAIN; 193 277 Saposin-like type B.2.
 FT DOMAIN; 307 388 Saposin-like type B.3.
 FT DOMAIN; 399 480 Saposin-like type B.4.
 FT DOMAIN; 485 518 Saposin-like type A.2.
 FT DISULFID; 64 139 By similarity.
 FT DISULFID; 67 133 By similarity.
 FT DISULFID; 95 107 By similarity.
 FT DISULFID; 197 273 By similarity.
 FT DISULFID; 200 267 By similarity.
 FT DISULFID; 229 240 By similarity.
 FT DISULFID; 311 384 By similarity.
 FT DISULFID; 314 378 By similarity.
 FT DISULFID; 342 353 By similarity.
 FT DISULFID; 403 476 By similarity.
 FT DISULFID; 406 470 By similarity.
 FT DISULFID; 434 445 By similarity.
 FT CARBOHYD; 81 81 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD; 214 214 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD; 328 328 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD; 420 420 N-linked (GlcNAc...) (Potential).
 FT CONFLICT; 94 94 R -> T (in Ref. 2).
 FT CONFLICT; 486 486 E -> D (in Ref. 2).
 SQ SEQUENCE 518 AA; 57601 MW; B803000E891C3963 CRC64;

Query Match 60.2%; Score 1679.5; DB 1; Length 518;
 Best Local Similarity 57.4%; Pred. No. 8e-100;
 Matches 301; Conservative 96; Mismatches 114; Indels 13; Gaps 5;
 QY 4 LFLASLIGALAGPVLGLKECTGSAVNCQVKTASDCGAVKHCLOTVMNKPTVKSLPC 63
 Db 5 LTLGLLAAAVASGVLWQKDCAGPEVWCQSLRTASQCGAVKHCQQNVWSKPAVNSIPC 64


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RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063994; AAH63994.1; -.
DR ZFIN; ZDB-GENE-020108-1; psap.
DR GO; GO:0005764; C:lysosome; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR GO; GO:0007585; P:respiratory gaseous exchange; IEA.
DR GO; GO:0006665; P:sphingolipid metabolism; IEA.
DR InterPro; IPR003119; Sapa.
DR InterPro; IPR007856; SApB.1.
DR InterPro; IPR008138; SApB.2.
DR InterPro; IPR008140; SApB_sub.
DR InterPro; IPR008373; SaposinB.
DR InterPro; IPR008139; Saposin.
DR InterPro; IPR011001; Saposin_like.
DR InterPro; IPR008137; Surfactant_B.
DR Pfam; PF02199; SApA.2.
DR Pfam; PF05184; SApB.1; 3.
DR Pfam; PF03489; SApB.2; 4.
DR PRINTS; PR01797; SAPOSIN.
DR ProDom; PD001732; SApB_sub.2.
DR ProDom; PD008002; Surfactant_B.1.
DR SMART; SM00162; SApA.2.
DR SMART; SM00162; SApA.2.
DR SEQUENCE 520 AA; 57444 MW; 91D35DB81A1ED6DC CRC64;

Query Match 50.6%; Score 1411; DB 2; Length 520;
Best Local Similarity 46.7%; Pred. No. 1.5e-82;
Matches 247; Conservative 120; Mismatches 144; Indels 18; Gaps 8;

QY 4 LFLASLIGALAGPVLGKCTRSAGVNCQVKTASDCGAVKCHLOTVMNKPTVKSLPC 63
DB 2 MLLTLLVTTAVASPLLGTEQCARGPPYWCQNVKTASLCGAVQHCCQNVNKNPQMKTVPC 61

QY 64 DICKDVVTAAGDMLKDNATEEILVLEKTCDWLPKPNNSASCKEIVDSYLPVLIDIKG 123
DB 62 DLCEVLVVVQQLKNDVTESELLGYLEKACQLIPDEGLANQCKEIVTTTQFSWASSKG 121

QY 124 EMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPBLDMTEVVVAPFMANIPLLYPQD 183
DB 122 ELDDPGVCGALGLCVSQAAALA-----KAQLTSNEIPQVDLNQVRVSPFLNIPQLLYPEE 177

QY 184 GPRSPQPKDGVDCQDCIQWTDITQAVRTNSTFVQALVEHVKECDRLGPGMADICKN 243
DB 178 ---KRETPKQKGDVDCQDCVTFISDTQDEARVNSSPFTNLLAQVENQCELLGPGMSDMCKE 234

QY 244 YISQYSEIAIOMMHPQKEICALGVGC-DEVKEMPOTLTPAK-VASKNVIPLALELVEP 301
DB 235 YISQYGLVPLVQQLMSMQPADIARAGCFPTKQKSVPMKELLPAKSIAPVAKFPVAVKEP 294

```

RESULT 14

```

Q9DGG82 PRELIMINARY; PRT; 522 AA.
ID Q9DGG82;
AC Q9DGG82;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Prosaposin.
GN Name=psap;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Altman N., Horowitz M.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF108655; AAG32919.1; -.
DR HSSP; Q92739; IN69.
DR ZFIN; ZDB-GENE-020108-1; psap.
DR GO; GO:0005764; C:lysosome; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR GO; GO:0007585; P:respiratory gaseous exchange; IEA.
DR GO; GO:0006685; P:sphingolipid metabolism; IEA.
DR InterPro; IPR003119; Sapa.
DR InterPro; IPR007856; SApB.1.
DR InterPro; IPR008138; SApB.2.
DR InterPro; IPR008140; SApB_sub.
DR InterPro; IPR008373; Saposin.
DR InterPro; IPR008139; SaposinB.
DR InterPro; IPR011001; Saposin_like.
DR InterPro; IPR008137; Surfactant_B.
DR Pfam; PF02199; SApA.2.
DR Pfam; PF05184; SApB.1; 3.
DR Pfam; PF03489; SApB.2; 4.
DR PRINTS; PR01797; SAPOSIN.
DR ProDom; PD001732; SApB_sub.2.
DR ProDom; PD008002; Surfactant_B.1.
DR SMART; SM00162; SApA.2.
DR SMART; SM00162; SApA.2.
DR SMART; SM00741; SApB.4.
DR SEQUENCE 522 AA; 57671 MW; D3C15A305725C1CD CRC64;

Query Match 48.2%; Score 1343; DB 2; Length 522;
Best Local Similarity 45.4%; Pred. No. 3.5e-78;
Matches 241; Conservative 117; Mismatches 153; Indels 20; Gaps 9;

QY 4 LFLASLIGALAGPVLGKCTRSAGVNCQVKTASDCGAVKCHLOTVMNKPTVKSLPC 63
DB 2 MLLTLLVTTAVASPLLGTEQCARGPPYWCQNVKTASLCGAVQHCCQNVNKNPQMKTVPC 61

QY 64 DICKDVVTAAGDMLKDNATEEILVLEKTCDWLPKPNNSASCKEIVDSYLPVLIDIKG 123
DB 62 DLCEVLVVVQQLKNDVTESELLGYLEKACQLIPDEGLANQCKEIVTTTQFSWASSKG 121

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2005, 11:22:35 ; Search time 167 Seconds
(without alignments)
1213.548 Million cell updates/sec

Title: US-09-743-684A-1
Perfect score: 2789
Sequence: 1 MYALFLASLIGALAGPVL.....NTETAACQNAVECHKRHWN 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1:	Geneseqp1980s:*
2:	Geneseqp1990s:*
3:	Geneseqp2000s:*
4:	Geneseqp2001s:*
5:	Geneseqp2002s:*
6:	Geneseqp2003as:*
7:	Geneseqp2003bs:*
8:	Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2789	100.0	524	2	AAR70783 Prosaposi
2	2789	100.0	524	2	AAW85652 Human pro
3	2789	100.0	524	3	AAW58716 Human pro
4	2789	100.0	524	6	AAW79099 Lip-TAA b
5	2789	100.0	524	6	ABU05200 Human exp
6	2789	100.0	524	6	ABU05207 Human exp
7	2789	100.0	524	6	ABU05203 Human exp
8	2789	100.0	524	6	ABU07340 Human exp
9	2789	100.0	524	6	ABU05216 Human exp
10	2789	100.0	524	6	ABU05202 Human exp
11	2789	100.0	524	6	ABU05214 Human exp
12	2789	100.0	524	6	ABU05215 Human exp
13	2789	100.0	524	6	ABU05199 Human exp
14	2789	100.0	524	6	ABU05212 Human exp
15	2789	100.0	524	6	ABU05213 Human exp
16	2789	100.0	524	6	ABU05205 Human exp
17	2789	100.0	524	7	ADF43340 Superanti
18	2789	100.0	524	7	ADJ69401 Human hea
19	2789	100.0	524	8	ADO08060 Human pol
20	2789	100.0	524	8	ADQ94328 Human pro
21	2789	100.0	524	8	ABM81149 Tumour-as
22	2779	99.6	524	6	ABU05208 Human exp
23	2777.5	99.6	527	4	AA31915 Amino aci
24	2777.5	99.6	527	5	ABP68602 Human pan
25	2777.5	99.6	527	6	ABU79100 Lip-TAA b

26	2777.5	99.6	527	6	ABU05204	Human exp
27	2777.5	99.6	527	6	ABU05210	Human exp
28	2777.5	99.6	527	7	ADF43341	Superanti
29	2772.5	99.4	523	4	AA31916	Amino aci
30	2772.5	99.4	523	6	ABU05211	Human exp
31	2768	99.2	526	6	ABU05209	Human exp
32	2767.5	99.2	527	6	ABU05206	Human exp
33	2449.5	87.8	479	6	ABR39442	Human GEN
34	2024.5	72.6	385	7	ABR41750	Human DIT
35	1969	70.6	554	7	ADB85295	Rat tubul
36	1921	68.9	554	5	ABW57102	Mouse isc
37	1293.5	46.4	268	8	ADP29875	Human sec
38	1201	43.1	521	3	AAW56966	Human SBP
39	1201	43.1	521	4	AAW78587	Human pro
40	1201	43.1	521	4	AAW79571	Human pro
41	1201	43.1	521	4	AAW86362	Human pro
42	1201	43.1	521	5	AAE15547	Human sec
43	1201	43.1	521	8	ADP30172	Human sec
44	1196	42.9	521	4	AAW79572	Human pro
45	1151.5	41.3	227	8	ADO57419	Hairless
46	1149	41.2	582	8	ADP30173	Human sec
47	1139.5	40.9	531	4	AAE01770	Human gen
48	1139.5	40.9	531	5	ABG64156	Human alb
49	1139.5	40.9	531	8	ADL77421	Albumin f
50	1125	40.3	210	6	ABU05201	Human exp
51	1093	39.2	209	5	ABG70166	Human pro
52	1023	36.7	483	8	ADP30415	Human sec
53	846	30.3	398	8	ADP30171	Human sec
54	834.5	29.9	362	4	AAW78588	Human pro
55	834.5	29.9	362	5	ABW07499	Human lip
56	812	29.1	153	6	ABU70504	Human adi
57	811	29.1	153	6	ABU70799	Human adi
58	676	24.2	129	6	ABU70422	Human adi
59	552	19.8	953	4	ABW58389	Drosophil
60	552	19.8	953	8	ADO08059	Fly polyo
61	545	19.5	241	7	ADM05844	Human pro
62	535.5	19.3	156	3	AAW58936	Breast an
63	537.5	19.3	345	4	AAE01850	Human gen
64	426.5	15.3	85	4	AA31912	Amino aci
65	414.5	14.9	83	4	AAW31929	Amino aci
66	412	14.8	80	2	AAR70784	Sapoisin-C
67	412	14.8	80	2	AAW85653	Human sap
68	412	14.8	80	4	AAU05697	Human Sap
69	412	14.8	80	7	ABU62252	Sphingolip
70	412	14.8	80	8	ADQ94329	Human pro
71	412	14.8	592	4	AAU05698	Human glu
72	355.5	12.7	381	1	AAW82934	SAP (Phe)
73	351.5	12.6	381	7	ADW67895	Human lun
74	350.5	12.6	381	1	AAW94756	Sequence
75	350.5	12.6	381	2	AAW06332	Human alv
76	350.5	12.6	381	3	AAW57152	Human sur
77	350.5	12.6	381	3	AAW97377	Human sur
78	350.5	12.6	381	4	AAW31913	Amino aci
79	350.5	12.6	381	8	ADG25258	Human pul
80	349.5	12.5	381	1	AAW70664	6kd pulmo
81	349.5	12.5	381	3	AAW78944	Human SP-
82	349.5	12.5	381	7	ADW70318	Surfactan
83	349.5	12.5	381	7	ADN39905	Cancer/an
84	349.5	12.5	381	8	ADJ37097	Human mal
85	347.5	12.5	381	1	AAW70438	Sequence
86	347.5	12.5	382	1	AAW82982	Human SP1
87	346.5	12.4	381	2	AAW05093	Gene prod
88	346.5	12.4	381	2	AAW14446	Pulmonary
89	335.5	12.0	381	2	AAW04833	Includes
90	335	12.0	380	4	AAW31917	Amino aci
91	327	11.7	61	2	AAW18584	Universal
92	327	11.7	69	2	AAW33258	Human pro
93	322.5	11.6	379	4	AAW31914	Amino aci
94	313	11.2	363	1	AAW70437	Sequence
95	292.5	10.5	370	8	ADL91125	Rabbit lu
96	268.5	9.6	257	3	AAW78942	Alveolar
97	266.5	9.6	256	3	AAW78945	Synthetic
98	244.5	8.8	362	2	AAW04211	Deduced a

99 239.5 8.6 60 2 AAW18583 Universal
100 239.5 8.6 60 2 AAY33260 Avian pro

ALIGNMENT'S

RESULT 1
AAR70783
XX AAR70783 standard; protein; 524 AA.
AC AAR70783;
XX AC
XX DT 25-MAR-2003 (revised)
XX DT 30-AUG-1995 (first entry)
XX DT
XX DE Prosaposin.
XX KW Saposin-C; neuron; myelination; nervous system; neuroblastoma;
KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;
KW adrenal leukodystrophy; prosaposin.
XX KW
XX OS Homo sapiens.
XX PN WO9503821-A1.
XX PD 09-FEB-1995.
XX PF 28-JUL-1994; 94WO-US008453.
XX PR 30-JUL-1993; 93US-00100247.
XX PR 21-APR-1994; 94US-00232513.
XX PA (OBRI/) O'BRIEN J S.
XX PI O'brien JS, Kishimoto Y;
XX PI WPI; 1995-082029/11.
XX DR N-PSDB; AAQ85355.
XX PT Stimulating neural cell out-growth and myelination - with pro:saposin,
PT saposin C or new neurotrophic peptide(s) from cytokine(s), for treating
PT nervous system diseases.
XX PS Disclosure; Page 30-32; 50pp; English.
XX CC The peptide given in AAR70773, corresponding to amino acids 8-29 of human
CC saposin-C (AAR70784), promotes neurite outgrowth in vitro. A consensus
CC sequence was determined by comparing the peptide with hematopoietic and
CC neurotrophic cytokines, and neurotrophic peptides (AAR70774-82) were
CC identified in the AB loop of human ciliary neurotrophic factor,
CC interleukins-6, -2, -3 and -gamma, erythropoietin and leukocyte
CC inhibitory factor, and in helix C of human interleukin-1-beta and
CC oncostatin-M. Prosaposin (AAR70783) and saposin-C also promoted nerve
CC cell myelination ex vivo. (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
XX correct PI field.)
XX SQ Sequence 524 AA;
Query Match 100.0%; Score 2789; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 4e-237;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYAFLLASLLGAALAGPVGLGKETRGSAVVCQNVKTASDCGAVKHCLQTVWVKPTVKS 60
DB 1 MYAFLLASLLGAALAGPVGLGKETRGSAVVCQNVKTASDCGAVKHCLQTVWVKPTVKS 60
QY 61 LPDCICKDVVTAAGDMLKDNATEEILVYLEKTDMLPKPNMSASCKEIVDSYLPVILDI 120
DB 61 LPDCICKDVVTAAGDMLKDNATEEILVYLEKTDMLPKPNMSASCKEIVDSYLPVILDI 120
QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILLY 180

DB 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILLY 180
QY 181 PDGPRSKPQPKONGDVCQDCIQWVTDIQTAVRTNSTFVQALVHVKEECDRLGPGMADI 240
DB 181 PDGPRSKPQPKONGDVCQDCIQWVTDIQTAVRTNSTFVQALVHVKEECDRLGPGMADI 240
QY 241 CKNYISOYSEIAIOMMMHMQPKETCALVGFCDCEKEMPOTLVPKASKNVIPALELVE 300
DB 241 CKNYISOYSEIAIOMMMHMQPKETCALVGFCDCEKEMPOTLVPKASKNVIPALELVE 300
QY 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKWCCKLPSKLSSECEQEV 360
DB 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKWCCKLPSKLSSECEQEV 360
QY 361 VDTYGSSILSILBEVSPELVCSMLHLCGSTRLPALTVHVTQPKDGGFCFVCKKLVGYLD 420
DB 361 VDTYGSSILSILBEVSPELVCSMLHLCGSTRLPALTVHVTQPKDGGFCFVCKKLVGYLD 420
QY 421 RNLEKNTKQETLAALKEGCSFLPDYKQCDQFVAEYEPVLIEILVEVMDPSPFVCLKIG 480
DB 421 RNLEKNTKQETLAALKEGCSFLPDYKQCDQFVAEYEPVLIEILVEVMDPSPFVCLKIG 480
QY 481 ACPSAHKPELLGTEKCIWGPSYWCQNTETAACQNAVEHCKRHVMN 524
DB 481 ACPSAHKPELLGTEKCIWGPSYWCQNTETAACQNAVEHCKRHVMN 524
RESULT 2
AAW85652
ID AAW85652 standard; protein; 524 AA.
XX AC AAW85652;
XX DT 19-JUL-1999 (first entry)
XX DE Human prosaposin N-terminal peptide.
XX KW Prosaposin; saposin; prosaptides; prosaposin receptor agonists; PRA;
KW peripheral nervous system; central nervous system; PNS; CNS; Akt; Bcl-2;
KW therapy; treatment; apoptosis; caspase; tumour necrosis factor; TNF;
KW cytokine; interferon gamma; IFN; inflammation; rheumatoid arthritis;
KW Crohn's disease; irritable bowel syndrome; asthma; cardiac infarction;
KW congestive heart failure; multiple sclerosis;
KW acute disseminated inflammatory leukoencephalitis;
KW progressive multifocal leukoencephalitis; Alzheimer's disease;
KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
KW ischemic heart disease; Guillain-Barre disease; alopecia; AIDS dementia;
KW cerebral malaria; HTLV; neuropathy;
KW inflammatory neurodegenerative disease; toxin-induced liver disease.
XX OS Homo sapiens.
XX XN WO9912559-A1.
XX PD 18-MAR-1999.
XX PF 09-SEP-1998; 98WO-US019216.
XX PR 09-SEP-1997; 97US-0058352P.
XX PR 04-JUN-1998; 98US-0088129P.
XX PA (REGC) UNIV CALIFORNIA.
XX PI O'brien JS;
XX DR WPI; 1999-229139/19.
XX DR N-PSDB; AAX08488.
XX PT Use of prosaposin receptor agonist.
XX PS Claim 7; Fig 2; 90pp; English.

CC Proasoposin is a 70kDa glycoprotein which is proteolytically processed to
CC generate saposins A, B, C and D, each of which are similar to each other
CC and have a similar placement of six cysteines, a glycosylation site and
CC conserved proline residues. Proasoposin, saposin C and proasoposin derived
CC peptides (proasoposins), have therapeutic applications in promoting
CC recovery after toxic, traumatic, myocardial ischaemic, degenerative and
CC inherited lesions to the peripheral and central nervous system.
CC Proasoposin receptor agonists (PRAs) inhibit proinflammatory cytokine-
CC induced apoptosis by activation of the Ser/Thr protein kinase Akt. Akt
CC dissociates complexes of Bcl-2 family members, such as BAD-Bcl-2,
CC releasing Bcl-2 and its family members which inhibit caspases, thereby
CC inhibiting apoptosis. An additional mechanism whereby PRAs inhibit
CC apoptosis is by blocking activation of JNK, a proapoptotic signaling
CC component. Within several minutes after binding to the receptor, PRAs
CC block JNK activation induced by tumor necrosis factor-alpha (TNF alpha).
CC The activation of JNK by TNF alpha is another well known mechanism for
CC TNF alpha-induced, as well as other proinflammatory cytokine-induced
CC apoptosis. The method can be used for inhibiting apoptosis which is
CC caspase-mediated or induced by a proinflammatory cytokine, for example
CC TNF alpha or interferon-gamma. It can be used for inhibiting apoptosis
CC associated with a disorder such as e.g. rheumatoid arthritis, Crohn's
CC disease, irritable bowel syndrome, asthma, cardiac infarction, congestive
CC heart failure, multiple sclerosis, acute disseminated inflammatory
CC leukoencephalitis, progressive multifocal leukoencephalitis, Alzheimer's
CC disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
CC disease, ischemic heart disease, Guillain-Barre disease, traumatic brain
CC injury, traumatic spinal cord injury, alopecia, AIDS dementia, cerebral
CC malaria, HTLV, neuropathy, inflammatory neurodegenerative disease, and
CC toxin-induced liver disease. This 524 N-terminal peptide of proasoposin
CC also acts as a proasoposin receptor agonist

XX Sequence 524: AA;

Query Match 100.0%; Score 2789; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 4e-237;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYALFLASLLGAALAGPVGLGKETRGSAVWCQNVKTASDCGAVKHCLQTVWNNKPTVKS 60
Db 1 MYALFLASLLGAALAGPVGLGKETRGSAVWCQNVKTASDCGAVKHCLQTVWNNKPTVKS 60

Qy 61 LPCDICKDVVTAAGDMLKDNATEEILVYLEKTCMDLPKPNNSACKEIVDSYLPVLDI 120
Db 61 LPCDICKDVVTAAGDMLKDNATEEILVYLEKTCMDLPKPNNSACKEIVDSYLPVLDI 120

Qy 121 IKGMSRPGVCVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFWANIPILLY 180
Db 121 IKGMSRPGVCVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFWANIPILLY 180

Qy 181 PDGPRSKPQKNGDVCDCIQMTVDIQTAVRTNSTFQVALVEHVEECEDRLGPGMADI 240
Db 181 PDGPRSKPQKNGDVCDCIQMTVDIQTAVRTNSTFQVALVEHVEECEDRLGPGMADI 240

Qy 241 CKNYISQYSEITAIQMMHMQPEIKALVGFCDVEKEMPQTLVPKAKSKNVPALVELVE 300
Db 241 CKNYISQYSEITAIQMMHMQPEIKALVGFCDVEKEMPQTLVPKAKSKNVPALVELVE 300

Qy 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMSKLPKSLSECEQEV 360
Db 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMSKLPKSLSECEQEV 360

Qy 361 VDTYSSILSILLESVSPVCSMLHLCSTGRLPALTVHTVTPQKDGGFCEVCKKLGVYLD 420
Db 361 VDTYSSILSILLESVSPVCSMLHLCSTGRLPALTVHTVTPQKDGGFCEVCKKLGVYLD 420

Qy 421 RNLEKNSKQETLAALAKGCSFLPDYQKQCDQFVAEYEPVLIELVEVMDPSFVCLKIG 480
Db 421 RNLEKNSKQETLAALAKGCSFLPDYQKQCDQFVAEYEPVLIELVEVMDPSFVCLKIG 480

Qy 481 ACPSAHKPLLGTEKICWGPSYWCQNTETAACQNAVEHCKRHVN 524
Db 481 ACPSAHKPLLGTEKICWGPSYWCQNTETAACQNAVEHCKRHVN 524

RESULT 3

RAY58716

ID AAY58716 standard; protein; 524 AA.

XX AAY58716;

XX AAY58716;

DT 25-APR-2000 (first entry)

DE Human prosaposin.

XX Prosaposin; saponin B; antiangiogenic; angiogenesis inhibitor;

KW anticancer; antiproliferative; antimigratory; Kaposi's sarcoma; tumour;

KW human; therapy.

XX Homo sapiens.

OS

FH Key

Protein

195..275

/note= "mature saposin B"

Peptide

195..205

/note= "specifically claimed antiangiogenic peptide of

Claim 23"

Peptide

196..200

/note= "specifically claimed antiangiogenic peptide of

Claim 4"

WO200002902-A1.

20-JAN-2000.

12-JUL-1999; 99WO-US015772.

13-JUL-1998; 98US-0092647P.

(GILL/) GILL P S.

Gill PS;

WPI; 2000-171128/15.

Saposin B derived peptides, useful as inhibitors of angiogenesis and

tumor growth.

Disclosure; Page 18; 78pp; English.

The present sequence is that of human prosaposin, a precursor of saposin

B. The invention is based on the discovery that saposin B, previously

known to be involved in the hydrolysis of sphingolipids, has potent

antiangiogenic and antitumor activity, and also has antiproliferative

and antimigratory activity against endothelial cells. This activity is

conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684

-715) which can be synthetically prepared and used in vitro or in vivo

for the treatment of undesired angiogenesis and tumor growth, especially

Kaposi's sarcoma (claimed). The polypeptides can also be used in

conjunction with cytotoxic moieties to selectively kill certain cell

types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma,

arteriovenous malformation, nonunion fracture, arthritis and other

connective tissue disorders, Osler-Weber syndrome, atherosclerotic

plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma,

retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma,

trachoma, vascular adhesions and hypertrophic scars

Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 3; Length 524;

Best Local Similarity 100.0%; Pred. No. 4e-237;

Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYALFLASLLGAALAGPVGLGKETRGSAVWCQNVKTASDCGAVKHCLQTVWNNKPTVKS 60

Db 1 MYALFLASLLGAALAGPVGLGKETRGSAVWCQNVKTASDCGAVKHCLQTVWNNKPTVKS 60

QY 61 LPDCICKDVVTAAGDMLKDNATEEELVYLEKTCMDLKPNNMSCKEIVDSYLPVILDI 120
 Db 61 LPDCICKDVVTAAGDMLKDNATEEELVYLEKTCMDLKPNNMSCKEIVDSYLPVILDI 120
 QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
 Db 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
 QY 181 PDGPRSRKPKQKNDGVDVCDQCIQMWTDIQTAVRTNSTFVQALVEHVKEECDRLGGMADI 240
 Db 181 PDGPRSRKPKQKNDGVDVCDQCIQMWTDIQTAVRTNSTFVQALVEHVKEECDRLGGMADI 240
 QY 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQMTLVPKAVSKNVIPALELVE 300
 Db 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQMTLVPKAVSKNVIPALELVE 300
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 Db 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCSPKLSLSECEQEV 360
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 Db 361 VDTYSSILSLLEEVSPVLCSMLHLCSTRLPALTVHVTQPKDGGFCVCKKLVGYLD 420
 QY 421 RNLEKNSTKQETILAALEKGCSPDPYQKQCDQFVAEYEPVLIELVEMDPSPFVCLKIG 480
 Db 421 RNLEKNSTKQETILAALEKGCSPDPYQKQCDQFVAEYEPVLIELVEMDPSPFVCLKIG 480
 QY 481 ACPSAHKPLLGTEKICWGPSYWCQNTETAACNAVEHCKRHVWN 524
 Db 481 ACPSAHKPLLGTEKICWGPSYWCQNTETAACNAVEHCKRHVWN 524

RESULT 4

ASU79099
 ID ABU79099 standard; protein; 524 AA.
 XX
 AC ABU79099;
 XX
 DT 18-JUN-2003 (first entry)
 XX
 DE Lip-TAA binding protein, Prosaposin.
 XX
 KW Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 KW gene therapy; mammalian cell receptor; cytostatic;
 KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
 KW tumouricidal immunocyte; antitumour.
 XX
 OS Unidentified.
 XX
 PN US2002177551-A1.
 XX
 XX 28-NOV-2002.
 PD
 XX 30-MAY-2001; 2001US-00870759.
 PF
 XX 31-MAY-2000; 2000US-0208128P.
 PR
 XX (TERM/) Terman D S.
 PA
 XX Terman DS;
 PI
 XX WPI; 2003-361759/34.
 DR
 XX
 XX
 PT A mammalian cell receptor, useful in the treatment of cancer by binding
 PT to tumor associated lipids where the binding induces anergy or apoptosis
 PT in T cells and antigen presenting cells.
 XX
 XX Disclosure; Page; 167pp; English.
 PS
 XX
 XX The invention relates to a mammalian cell receptor, useful in the
 CC treatment of cancer, which binds to tumour associated lipids and induces
 CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).
 CC

CC Also included are a mammalian cell useful in the treatment of cancer
 CC where the receptor which binds tumour associated lipids and induces
 CC cellular inactivation or death is deleted or functionally deactivated,
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 CC (by allowing tumour associated lipids to contact immunocytes in which
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 CC sphingolipids, glycosphingolipids, phosphoglycolipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 CC deleted); a construct useful in the treatment of cancer comprising a
 CC superantigen (Sag) nucleotide inserted into a virus, a mammalian T cell
 CC useful in the treatment of cancer (where an adaptor protein which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidally
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to
 CC contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidally activated population,
 CC and administering APCs to the host), producing a tumouricidal T cell
 CC population ex vivo in a mammal) by allowing a tumour associated lipids to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC administering the tumouricidally activated T cells to the host, or
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidally activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC receptors, methods and compositions are useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents a tumour antigen or a motif identifying a tumour
 CC antigen, which can be functionally deactivated in the method of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format from the
 CC US patent office website at
 CC "seqdata.uspto.gov/sequence.html?DocID=20020177551"

XX Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 6; Length 524;
 Best Local Similarity 100.0%; Pred. No. 4e-237;
 Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MYALFLLASLGAALAGPVLGLKECTRGSAVWCQNVKTASDCGAVKHCLQTVNKNPTVKS 60
 Db 1 MYALFLLASLGAALAGPVLGLKECTRGSAVWCQNVKTASDCGAVKHCLQTVNKNPTVKS 60
 QY 61 LPDCICKDVVTAAGDMLKDNATEEELVYLEKTCMDLKPNNMSCKEIVDSYLPVILDI 120
 Db 61 LPDCICKDVVTAAGDMLKDNATEEELVYLEKTCMDLKPNNMSCKEIVDSYLPVILDI 120
 QY 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
 Db 121 IKGEMSRPGEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
 QY 181 PDGPRSRKPKQKNDGVDVCDQCIQMWTDIQTAVRTNSTFVQALVEHVKEECDRLGGMADI 240
 Db 181 PDGPRSRKPKQKNDGVDVCDQCIQMWTDIQTAVRTNSTFVQALVEHVKEECDRLGGMADI 240
 QY 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQMTLVPKAVSKNVIPALELVE 300
 Db 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQMTLVPKAVSKNVIPALELVE 300

QY 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELDAPDKMCKLPSLSSECEQV 360
DB 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELDAPDKMCKLPSLSSECEQV 360
QY 361 VDTYSSILSILLESVPELVCSMLHLCGSGTFLPALTVHVTPQKDGGEVCKLVGYLD 420
DB 361 VDTYSSILSILLESVPELVCSMLHLCGSGTFLPALTVHVTPQKDGGEVCKLVGYLD 420
QY 421 RNLEKNSTKQELIAALEKGCSEFLPDYPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
DB 421 RNLEKNSTKQELIAALEKGCSEFLPDYPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
QY 481 ACPSAHKPLLGTEKICWGPSYWCQNTETAACNAVEHCKRHVWN 524
DB 481 ACPSAHKPLLGTEKICWGPSYWCQNTETAACNAVEHCKRHVWN 524

RESULT 5
ABU05200
ID ABU05200 standard; protein; 524 AA.
XX AC ABU05200;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1866.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.

PI Chiciz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX Example 2; SEQ ID NO 1866; 134pp; English.
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,

CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 524 AA;
Query Match 100.0%; Score 2789; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 4e-237;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYALFLASLLGALAGVPLGLKCTRGSAVWCQNVKTASDCGAVKHCLQTVNKPVTKS 60
DB 1 MYALFLASLLGALAGVPLGLKCTRGSAVWCQNVKTASDCGAVKHCLQTVNKPVTKS 60
QY 61 LPCDICKDVTAAGDMLKDNATEEELVYLEKTCMDLKPNNMSACKIEIVSLPVILDI 120
DB 61 LPCDICKDVTAAGDMLKDNATEEELVYLEKTCMDLKPNNMSACKIEIVSLPVILDI 120
QY 121 IKGEMSRPEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLY 180
DB 121 IKGEMSRPEVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLY 180
QY 181 PDGPRSKPQPKDNGDVQDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
DB 181 PDGPRSKPQPKDNGDVQDCIQMVTDIQTAVRTNSTFVQALVEHVKECDRLGPGMADI 240
QY 241 CKNIYSQYSEIATQMMHMQKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
DB 241 CKNIYSQYSEIATQMMHMQKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
QY 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELDAPDKMCKLPSLSSECEQV 360
DB 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKELDAPDKMCKLPSLSSECEQV 360
QY 361 VDTYSSILSILLESVPELVCSMLHLCGSGTFLPALTVHVTPQKDGGEVCKLVGYLD 420
DB 361 VDTYSSILSILLESVPELVCSMLHLCGSGTFLPALTVHVTPQKDGGEVCKLVGYLD 420
QY 421 RNLEKNSTKQELIAALEKGCSEFLPDYPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
DB 421 RNLEKNSTKQELIAALEKGCSEFLPDYPYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
QY 481 ACPSAHKPLLGTEKICWGPSYWCQNTETAACNAVEHCKRHVWN 524
DB 481 ACPSAHKPLLGTEKICWGPSYWCQNTETAACNAVEHCKRHVWN 524

RESULT 6
ABU05207
ID ABU05207 standard; protein; 524 AA.
XX AC ABU05207;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1873.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.

```
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1873; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 4e-237;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLASLLGAAAGVPLGLKECTRGSAVWCQNVKTASDCGAVKHCLQTVWPKPTVKS 60
Db 1 MYALFLASLLGAAAGVPLGLKECTRGSAVWCQNVKTASDCGAVKHCLQTVWPKPTVKS 60
QY 61 LPCDICKDVVTAAGDMLKDNATEBELLVLEKTCDWLPKPNMSASCKEIVDSYLPVLIDI 120
Db 61 LPCDICKDVVTAAGDMLKDNATEBELLVLEKTCDWLPKPNMSASCKEIVDSYLPVLIDI 120
QY 121 IKGMSRFGVCSALNLCESLQKHIAELNHQKLESNKIPELDMTEVVVAPFMANIPLLY 180
Db 121 IKGMSRFGVCSALNLCESLQKHIAELNHQKLESNKIPELDMTEVVVAPFMANIPLLY 180
QY 181 PQDGPRSPQKNDGVDCDQIMVTDIQTAVRTNSTFVQALVEHVHECECDRLGFMADI 240
Db 181 PQDGPRSPQKNDGVDCDQIMVTDIQTAVRTNSTFVQALVEHVHECECDRLGFMADI 240
QY 241 CKNYISQYSEIAQMMHMQPEIKCALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
Db 241 CKNYISQYSEIAQMMHMQPEIKCALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
QY 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCSKLPKSLSECEQEV 360
Db 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCSKLPKSLSECEQEV 360
QY 361 VDTYSSILSLILERSVPELVCSMLHLCSGTRLPALTTHVTPQKDGGEVCKKLVGLYD 420
Db 361 VDTYSSILSLILERSVPELVCSMLHLCSGTRLPALTTHVTPQKDGGEVCKKLVGLYD 420
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QY 421 RNLEKNSTKQIBLALEKGCSEFLDPYQKQCDQFVAEYEPVLIELVVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTKQIBLALEKGCSEFLDPYQKQCDQFVAEYEPVLIELVVEVMDPSFVCLKIG 480
QY 481 ACPSAHKPLLGTEKCIWGPSYWCQNTTETAACNAVEHCKRHWN 524
Db 481 ACPSAHKPLLGTEKCIWGPSYWCQNTTETAACNAVEHCKRHWN 524

RESULT 7
ABU05203
ID ABU05203 standard; protein; 524 AA.
XX
XX AC ABU05203;
XX
XX DT 29-JAN-2003 (first entry)
XX
XX DE Human expressed protein tag (EPT) #1869.
XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX OS Homo sapiens.
XX
XX FN WO200278524-A2.
XX
XX PD 10-OCT-2002.
XX
XX PP 28-MAR-2002; 2002WO-US009671.
XX
XX PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX PA (ZYCO-) ZYCOS INC.
XX
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX
XX DR WPI; 2003-040607/03.
XX
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX PS Example 2; SEQ ID NO 1869; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 524 AA;
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Query Match		100.0%; Score 2789; DB 6; Length 524;
Best Local Similarity		100.0%; Pred. No. 4e-237;
Matches 524; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MYAFLLASLLGAALAGPVLGLKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNNKPTVKS 60
Db	1	MYAFLLASLLGAALAGPVLGLKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNNKPTVKS 60
QY	61	LPCDICKDVVTAAGDMLKDNATEEILVYLEKTDMLPKPNNMSCKEIVDSYLPVILDI 120
Db	61	LPCDICKDVVTAAGDMLKDNATEEILVYLEKTDMLPKPNNMSCKEIVDSYLPVILDI 120
QY	121	IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
Db	121	IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
QY	181	PDGPRSKPQPKNGDVQCDCIQWTDIQTAVRTNSTFVQALVEHVKEECDRLGFGMADI 240
Db	181	PDGPRSKPQPKNGDVQCDCIQWTDIQTAVRTNSTFVQALVEHVKEECDRLGFGMADI 240
QY	241	CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
Db	241	CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
QY	301	PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLPKSLSECEQEV 360
Db	301	PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLPKSLSECEQEV 360
QY	361	VDTYGSSILSILLEVSPVCSMLHLCSGTRLPALTTHVTQPKDGGFCVCKKLGVYLD 420
Db	361	VDTYGSSILSILLEVSPVCSMLHLCSGTRLPALTTHVTQPKDGGFCVCKKLGVYLD 420
QY	421	RNLEKNSTKQEIILAALEKGCFLPDYQKQCDQFVAEYEPVLIETLVEMDPSFVCLKIG 480
Db	421	RNLEKNSTKQEIILAALEKGCFLPDYQKQCDQFVAEYEPVLIETLVEMDPSFVCLKIG 480
QY	481	ACPSAHKPELLGTEKICINGPSYWCQNTETATAACNAVEHCKRHWN 524
Db	481	ACPSAHKPELLGTEKICINGPSYWCQNTETATAACNAVEHCKRHWN 524
RESULT 8		
ID	ABU07340	
AC	ABU07340 standard; protein; 524 AA.	
XX	ABU07340;	
XX	29-JAN-2003 (first entry)	
XX	Human expressed protein tag (EPT) #2041.	
DE	Translational profiling; expressed protein tag; EPT; kinase; phosphatase;	
KW	protease; protease inhibitor; transporter; cytoskeletal protein;	
KW	receptor; transcription factor; cancer; MHC;	
KW	major histocompatibility complex; myeloma; colon cancer; gastric cancer;	
KW	adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.	
OS	Homo sapiens.	
XX	WO200278524-A2.	
PN	10-OCT-2002.	
XX	28-MAR-2002; 2002WO-US009671.	
PR	28-MAR-2001; 2001US-0279495P.	
PR	21-MAY-2001; 2001US-0292544P.	
PR	08-AUG-2001; 2001US-0310801P.	
PR	01-OCT-2001; 2001US-0326370P.	
PR	04-DEC-2001; 2001US-0336780P.	
PR	20-FEB-2002; 2002US-0358985P.	
XX	(ZYCO-) ZYCOS INC.	
PA		
XX	Chicz RM, Tomlinson AJ, Urban RG;	
PI	WPI; 2003-040607/03.	
XX	New polypeptides (e.g. kinases, phosphatases, proteases, transporters,	
PT	cytoskeletal proteins, receptors or transcription factors), useful for	
PT	treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or	
PT	leukemia.	
XX	Example 2; SEQ ID NO 2041; 134pp; English.	
XX	The invention describes a purified polypeptide, which comprises a	
CC	fragment of a kinase, phosphatase, protease, or protease inhibitor,	
CC	transporter, cytoskeletal protein, receptor or transcription factor. The	
CC	polypeptide is useful as an immunogenic composition for eliciting in a	
CC	mammal an immunogenic response directed against any of the purified	
CC	polypeptide. The purified polypeptide, or the antibody that binds to this	
CC	polypeptide, is useful for treating cancer. The polypeptide is also	
CC	useful for identifying compounds that binds to a naturally processed	
CC	class I or class II MHC-binding polypeptide. The polypeptides and	
CC	polynucleotides are particularly useful for treating or preventing	
CC	myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,	
CC	lymphoma or leukaemia. These are also useful for screening agents for	
CC	treating the above mentioned diseases. This sequence represents an	
CC	expressed protein tag (EPT) isolated from human tissue for translational	
CC	profiling. Note: This sequence does not appear in the printed	
CC	specification but was obtained in electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX	Sequence 524 AA;	
QY	1	MYAFLLASLLGAALAGPVLGLKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNNKPTVKS 60
Db	1	MYAFLLASLLGAALAGPVLGLKECTRGSAVWCNQVKTASDCGAVKHCLQTVWNNKPTVKS 60
QY	61	LPCDICKDVVTAAGDMLKDNATEEILVYLEKTDMLPKPNNMSCKEIVDSYLPVILDI 120
Db	61	LPCDICKDVVTAAGDMLKDNATEEILVYLEKTDMLPKPNNMSCKEIVDSYLPVILDI 120
QY	121	IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
Db	121	IKGMSRPGVCSALNLCESLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLLLY 180
QY	181	PDGPRSKPQPKNGDVQCDCIQWTDIQTAVRTNSTFVQALVEHVKEECDRLGFGMADI 240
Db	181	PDGPRSKPQPKNGDVQCDCIQWTDIQTAVRTNSTFVQALVEHVKEECDRLGFGMADI 240
QY	241	CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
Db	241	CKNYISQYSEIAIQMMHMQPKEICALVGFCDVEKEMPQTLVPAKVASKNVIPALELVE 300
QY	301	PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLPKSLSECEQEV 360
Db	301	PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLPKSLSECEQEV 360
QY	361	VDTYGSSILSILLEVSPVCSMLHLCSGTRLPALTTHVTQPKDGGFCVCKKLGVYLD 420
Db	361	VDTYGSSILSILLEVSPVCSMLHLCSGTRLPALTTHVTQPKDGGFCVCKKLGVYLD 420
QY	421	RNLEKNSTKQEIILAALEKGCFLPDYQKQCDQFVAEYEPVLIETLVEMDPSFVCLKIG 480
Db	421	RNLEKNSTKQEIILAALEKGCFLPDYQKQCDQFVAEYEPVLIETLVEMDPSFVCLKIG 480
QY	481	ACPSAHKPELLGTEKICINGPSYWCQNTETATAACNAVEHCKRHWN 524
Db	481	ACPSAHKPELLGTEKICINGPSYWCQNTETATAACNAVEHCKRHWN 524

XX PS Example 2; SEQ ID NO 1868; 134pp; English.

XX CC The invention describes a purified polypeptide, which comprises a

XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,

XX CC transporter, cytoskeletal protein, receptor or transcription factor. The

XX CC polypeptide is useful as an immunogenic composition for eliciting in a

XX CC mammal an immunogenic response directed against any of the purified

XX CC polypeptide. The purified polypeptide, or the antibody that binds to this

XX CC polypeptide, is useful for treating cancer. The polypeptide is also

XX CC useful for identifying compounds that binds to a naturally processed

XX CC class I or class II MHC-binding polypeptide. The polypeptides and

XX CC polynucleotides are particularly useful for treating or preventing

XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,

XX CC lymphoma or leukaemia. These are also useful for screening agents for

XX CC treating the above mentioned diseases. This sequence represents an

XX CC expressed protein tag (EPT) isolated from human tissue for translational

XX CC profiling. Note: This sequence does not appear in the printed

XX CC specification but was obtained in electronic format directly from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 6; Length 524;

Best Local Similarity 100.0%; Pred. No. 4e-237;

Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLASLLGALAGPVGLGKECTRGSAVVCQNVKTASDCGAVKHCLQTVNNKPTVKS 60

Db 1 MYALFLASLLGALAGPVGLGKECTRGSAVVCQNVKTASDCGAVKHCLQTVNNKPTVKS 60

QY 61 LPDCICKDVVTAAGDMLKDNATEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120

Db 61 LPDCICKDVVTAAGDMLKDNATEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120

QY 121 IKGMSRPGEVCSALNLCESLQKHAEHLNQHQLSNNKIPELDMTEVAVPFMANIPLLY 180

Db 121 IKGMSRPGEVCSALNLCESLQKHAEHLNQHQLSNNKIPELDMTEVAVPFMANIPLLY 180

QY 181 PODGPRSKPQKPDNGDVCDCLQWTDIQTAVRTNSTFFVQALVEHVKECDRLGPMADI 240

Db 181 PODGPRSKPQKPDNGDVCDCLQWTDIQTAVRTNSTFFVQALVEHVKECDRLGPMADI 240

QY 241 CKNYISQYSEIAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKASKNVIPALELVE 300

Db 241 CKNYISQYSEIAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKASKNVIPALELVE 300

QY 301 PIKKEVPKASDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKWCSPKLSSECEQEV 360

Db 301 PIKKEVPKASDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKWCSPKLSSECEQEV 360

QY 361 VDTYGSILSILLEEVSPELVCSMLHLCSGTRLPALT/VHVTQPKDGGFCEVCCKLVGYLD 420

Db 361 VDTYGSILSILLEEVSPELVCSMLHLCSGTRLPALT/VHVTQPKDGGFCEVCCKLVGYLD 420

QY 421 RNLEKNSTQKIELALEKCSFLPDYQKQDOFVAEYEPVLIIEILVEVMDPSFVCLKIG 480

Db 421 RNLEKNSTQKIELALEKCSFLPDYQKQDOFVAEYEPVLIIEILVEVMDPSFVCLKIG 480

QY 481 ACPSAHKPLLGTEKCIWGPSYQNTETAAQCNVAHECHKRHYNN 524

Db 481 ACPSAHKPLLGTEKCIWGPSYQNTETAAQCNVAHECHKRHYNN 524

RESULT 11

ABU05214

ID ABU05214 standard; protein; 524 AA.

XX AC ABU05214;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1880.

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

XX KW protease; protease inhibitor; transporter; cytoskeletal protein;

XX KW receptor; transcription factor; cancer; MHC;

XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;

XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAY-2001; 2001US-0279495P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0328370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,

XX cytoskeletal proteins, receptors or transcription factors), useful for

XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or

XX leukemia.

XX Example 2; SEQ ID NO 1880; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a

XX fragment of a kinase, phosphatase, protease, protease inhibitor,

XX transporter, cytoskeletal protein, receptor or transcription factor. The

XX polypeptide is useful as an immunogenic composition for eliciting in a

XX mammal an immunogenic response directed against any of the purified

XX polypeptide. The purified polypeptide, or the antibody that binds to this

XX polypeptide, is useful for treating cancer. The polypeptide is also

XX useful for identifying compounds that binds to a naturally processed

XX class I or class II MHC-binding polypeptide. The polypeptides and

XX polynucleotides are particularly useful for treating or preventing

XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,

XX lymphoma or leukaemia. These are also useful for screening agents for

XX treating the above mentioned diseases. This sequence represents an

XX expressed protein tag (EPT) isolated from human tissue for translational

XX profiling. Note: This sequence does not appear in the printed

XX specification but was obtained in electronic format directly from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 6; Length 524;

Best Local Similarity 100.0%; Pred. No. 4e-237;

Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLASLLGALAGPVGLGKECTRGSAVVCQNVKTASDCGAVKHCLQTVNNKPTVKS 60

Db 1 MYALFLASLLGALAGPVGLGKECTRGSAVVCQNVKTASDCGAVKHCLQTVNNKPTVKS 60

QY 61 LPDCICKDVVTAAGDMLKDNATEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120

Db 61 LPDCICKDVVTAAGDMLKDNATEEILVYLEKTCDWLPKPNMSASCKEIVDSYLPVLDI 120

QY 121 IKGMSRPGEVCSALNLCESLQKHAEHLNQHQLSNNKIPELDMTEVAVPFMANIPLLY 180

Db 121 IKGMSRPGEVCSALNLCESLQKHAEHLNQHQLSNNKIPELDMTEVAVPFMANIPLLY 180

QY 181 PODGPRSKPQKPDNGDVCDCLQWTDIQTAVRTNSTFFVQALVEHVKECDRLGPMADI 240

Db 181 PDGPRSKPQKNDGVCQDCIQMTDITQAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
Qy 241 CKNYISQYSETAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVI PALELVE 300
Db 241 CKNYISQYSETAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVI PALELVE 300
Qy 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQEV 360
Db 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQEV 360
Qy 361 VDTYSSILSLLEEVSPELVCSMLHLCSGTRLPALTTHVTQPKDGGFCEVCKKLVGYLD 420
Db 361 VDTYSSILSLLEEVSPELVCSMLHLCSGTRLPALTTHVTQPKDGGFCEVCKKLVGYLD 420
Qy 421 RNLEKNSTKQEILAALEKGCFLPDYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTKQEILAALEKGCFLPDYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Qy 481 ACPSAHKPELLGTEKICWGPSYWCQNTETAACNAVEHCCKRHVN 524
Db 481 ACPSAHKPELLGTEKICWGPSYWCQNTETAACNAVEHCCKRHVN 524

RESULT 12
ABU05215
ID ABU05215 standard; protein; 524 AA.
XX AC ABU05215;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1881.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 1881; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this

CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 4e-23;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYALFLLASLLGAALAGFVLGLKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
Db 1 MYALFLLASLLGAALAGFVLGLKECTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60

Qy 61 LPDCICKDVVTAAGDMLKDNATEEILVYLEKTCMDLWPKPNMSASCKEIVDSYLPVILDI 120
Db 61 LPDCICKDVVTAAGDMLKDNATEEILVYLEKTCMDLWPKPNMSASCKEIVDSYLPVILDI 120

Qy 121 IKGEMSRPGEVCSALNLCESLQKHLAEINHQLESNKIPELDMTEVVAPPMANIPLLLY 180
Db 121 IKGEMSRPGEVCSALNLCESLQKHLAEINHQLESNKIPELDMTEVVAPPMANIPLLLY 180

Qy 181 PDGPRSKPQKNDGVCQDCIQMTDITQAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
Db 181 PDGPRSKPQKNDGVCQDCIQMTDITQAVRTNSTFVQALVEHVKEECDRLGPGMADI 240

Qy 241 CKNYISQYSETAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVI PALELVE 300
Db 241 CKNYISQYSETAIQMMHMQPKIEICALVGFCDVEKEMPQTLVPAKVASKNVI PALELVE 300

Qy 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQEV 360
Db 301 PIKKEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMCCKLPKSLSECEQEV 360

Qy 361 VDTYSSILSLLEEVSPELVCSMLHLCSGTRLPALTTHVTQPKDGGFCEVCKKLVGYLD 420
Db 361 VDTYSSILSLLEEVSPELVCSMLHLCSGTRLPALTTHVTQPKDGGFCEVCKKLVGYLD 420

Qy 421 RNLEKNSTKQEILAALEKGCFLPDYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480
Db 421 RNLEKNSTKQEILAALEKGCFLPDYQKQCDQFVAEYEPVLIEILVEVMDPSFVCLKIG 480

Qy 481 ACPSAHKPELLGTEKICWGPSYWCQNTETAACNAVEHCCKRHVN 524
Db 481 ACPSAHKPELLGTEKICWGPSYWCQNTETAACNAVEHCCKRHVN 524

RESULT 13
ABU05199
ID ABU05199 standard; protein; 524 AA.
XX AC ABU05199;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1865.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX

CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 4e-237;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLASLLGAALAGPVLGKCTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
DB 1 MYALFLASLLGAALAGPVLGKCTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60

QY 61 LPCDICKDVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
DB 61 LPCDICKDVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120

QY 121 IKGEMSRPGEVCSALNLCSLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILLY 180
DB 121 IKGEMSRPGEVCSALNLCSLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILLY 180

QY 181 PDGPRSRKPOKNGDVQCDCIQMVTDTQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
DB 181 PDGPRSRKPOKNGDVQCDCIQMVTDTQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240

QY 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDEVKEMPQTLVPAKASKNVI PALELVE 300
DB 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDEVKEMPQTLVPAKASKNVI PALELVE 300

QY 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMSCKLPKSLSEECQEV 360
DB 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMSCKLPKSLSEECQEV 360

QY 361 VDTYSSILSLLEEVSPELVCSMLHLCSTGTRLPALT VHVTQPKDGGCFCEVCKKLGVYLD 420
DB 361 VDTYSSILSLLEEVSPELVCSMLHLCSTGTRLPALT VHVTQPKDGGCFCEVCKKLGVYLD 420

QY 421 RNLEKNSTKQEILAALEKGCSPDPYQKQCDQFVAEYEPVLIETILVEVMDPSFVCLKIG 480
DB 421 RNLEKNSTKQEILAALEKGCSPDPYQKQCDQFVAEYEPVLIETILVEVMDPSFVCLKIG 480

QY 481 ACPSAHKPLLTGTEKICWGPSYWCQNTETAACQNAVEHCCKRHWN 524
DB 481 ACPSAHKPLLTGTEKICWGPSYWCQNTETAACQNAVEHCCKRHWN 524

RESULT 15
ABU05213
AC ABU05213 standard; protein; 524 AA.
XX AC ABU05213;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1879.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCO INC.
XX PA Chicx RM, Tomlinson AJ, Urban RG;
XX PI WPI; 2003-040607/03.
XX DR
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1879; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, or protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 524 AA;

Query Match 100.0%; Score 2789; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 4e-237;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYALFLASLLGAALAGPVLGKCTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60
DB 1 MYALFLASLLGAALAGPVLGKCTRGSAVWCQNVKTASDCGAVKHCLQTVWNKPTVKS 60

QY 61 LPCDICKDVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120
DB 61 LPCDICKDVVTAAGDMLKDNATEEELVYLEKTCDWLPKPNMSASCKEIVDSYLPVILDI 120

QY 121 IKGEMSRPGEVCSALNLCSLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILLY 180
DB 121 IKGEMSRPGEVCSALNLCSLQKHLAELNHQKLESNKIPELDMTEVVAPFMANIPLILLY 180

QY 181 PDGPRSRKPOKNGDVQCDCIQMVTDTQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240
DB 181 PDGPRSRKPOKNGDVQCDCIQMVTDTQTAVRTNSTFVQALVEHVKEECDRLGPGMADI 240

QY 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDEVKEMPQTLVPAKASKNVI PALELVE 300
DB 241 CKNYISQYSEIAIQMMHMQPKEICALVGFCDEVKEMPQTLVPAKASKNVI PALELVE 300

QY 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMSCKLPKSLSEECQEV 360
DB 301 PIKHEVPAKSDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMSCKLPKSLSEECQEV 360

QY 361 VDTYSSILSLLEEVSPELVCSMLHLCSTGTRLPALT VHVTQPKDGGCFCEVCKKLGVYLD 420
DB 361 VDTYSSILSLLEEVSPELVCSMLHLCSTGTRLPALT VHVTQPKDGGCFCEVCKKLGVYLD 420

QY 421 RNLEKNSTKQEILAALEKGCSPDPYQKQCDQFVAEYEPVLIETILVEVMDPSFVCLKIG 480
DB 421 RNLEKNSTKQEILAALEKGCSPDPYQKQCDQFVAEYEPVLIETILVEVMDPSFVCLKIG 480

Oy 481 ACPSAHKPLLGTEKCIWGPSYWCNTETATAACNAVEHCKRHYWN 524
Db 481 ACPSAHKPLLGTEKCIWGPSYWCNTETATAACNAVEHCKRHYWN 524

Search completed: June 30, 2005, 11:32:37
Job time : 171 secs

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OM protein - protein search, using sw model

Run on: June 30, 2005, 11:36:37 ; Search time 31.2346 Seconds
(without alignments)
136.207 Million cell updates/sec

Title: US-09-743-684A-19

Perfect score: 63

Sequence: 1 GDVQCDCIQMW 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1053335

Minimum DB seq length: 0

Maximum DB seq length: 71

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A: Geneseq 16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	100.0	11	3	AAY58691 Antiangio
2	57	90.5	10	3	AAY58693 Antiangio
3	55	87.3	15	3	AAY58685 Antiangio
4	53	84.1	9	3	AAY58696 Antiangio
5	53	84.1	11	3	AAY58704 Antiangio
6	53	84.1	11	3	AAY58705 Antiangio
7	51	81.0	9	3	AAY58701 Antiangio
8	48	76.2	8	3	AAY58697 Antiangio
9	47	74.6	8	3	AAY58702 Antiangio
10	47	74.6	19	2	AAW18588 Antiangio
11	43	68.3	7	3	AAY58698 Antiangio
12	43	68.3	11	3	AAY58692 Antiangio
13	41	65.1	60	5	ADH32471 Yeast smo
14	40	63.5	15	2	AAW18587 Universal
15	40	63.5	22	7	ADE37012 Binding a
16	39	61.9	6	3	AAY58699 Antiangio
17	38	60.3	7	3	AAY58703 Antiangio
18	37	58.7	53	4	AAU45013 Propionib
19	37	58.7	53	6	AAW41532 Propionib
20	37	58.7	71	4	AAW40216 Human pol
21	37	58.7	71	4	AAW37337 Ring fing
22	36	57.1	31	5	AAO14371 Human met
23	35	55.6	56	4	AAW15618 Peptide #
24	35	55.6	56	4	ABB34623 Peptide #
25	35	55.6	56	4	AAW28116 Peptide #

26	35	55.6	56	4	ABB29447	Abb29447 Peptide #
27	35	55.6	56	4	ABB20033	Abb20033 Protein #
28	35	55.6	56	4	AAM67809	Aam67809 Human bon
29	35	55.6	56	4	AAM55413	Aam55413 Human bra
30	35	55.6	56	4	ABG49446	Abg49446 Human liv
31	35	55.6	56	4	AAM03362	Aam03362 Peptide #
32	35	55.6	56	5	ABG37352	Abg37352 Human pep
33	35	55.6	68	8	ADM41991	Adm41991 FYVE doma
34	35	55.6	70	3	AAG36901	Aag36901 Arabidops
35	34	54.0	12	1	AAP82485	Aap82485 Anticoagu
36	34	54.0	12	1	AAR34790	Aar34790 Anticoagu
37	34	54.0	24	1	AAP83186	Aap83186 Sequence
38	34	54.0	46	3	ABAB37384	Abab37384 Human sec
39	34	54.0	62	3	AAG05017	Aag05017 Arabidops
40	34	54.0	71	4	AAU41055	Aau41055 Propionib
41	34	54.0	71	6	ABM37574	Abm37574 Propionib
42	33	52.4	6	3	AAV58695	Aav58695 Antiangio
43	33	52.4	34	5	AAG80162	Aag80162 TPR2B pro
44	33	52.4	37	4	ABG15269	Abg15269 Novel hum
45	33	52.4	52	3	AAG09489	Aag09489 Arabidops
46	33	52.4	59	4	AAU55894	Aau55894 Propionib
47	33	52.4	59	6	ABM52413	Abm52413 Propionib
48	32	50.8	9	4	AAU27172	Aau27172 Hepsin pe
49	32	50.8	9	6	ADA16895	Ada16895 Human hep
50	32	50.8	9	7	ABE24875	Abe24875 Human hep
51	32	50.8	9	8	ADR18699	Adr18699 HLA A0201
52	32	50.8	29	3	AAO8256	Aao8256 Consensus
53	32	50.8	29	4	ABG28008	Abg28008 Novel hum
54	32	50.8	29	5	AAU10944	Aau10944 AGP-3 rel
55	32	50.8	54	4	AAU42805	Aau42805 Propionib
56	32	50.8	55	2	AAW53166	Aaw53166 Retrovira
57	32	50.8	55	6	ABP80559	Abp80559 N. gonorr
58	32	50.8	56	2	AAW53165	Aaw53165 Retrovira
59	32	50.8	56	2	AAW53167	Aaw53167 Retrovira
60	32	50.8	61	4	ABG01258	Abg01258 Novel hum
61	32	50.8	61	3	AAG01723	Aag01723 Human sec
62	32	50.8	63	3	ADL05263	Adl05263 M. catarr
63	32	50.8	67	8	AAU37400	Aau37400 Anticoagu
64	31	49.2	10	2	AAAB36847	Aaab36847 E. coli M
65	31	49.2	20	3	AAV41426	Aav41426 Fragment
66	31	49.2	30	2	AAV25848	Aav25848 Human sec
67	31	49.2	30	2	ABO58992	Abos58992 Human gen
68	31	49.2	44	8	AAV57176	Aav57176 Arabidops
69	31	49.2	45	3	AAAG60367	Aaag60367 Arabidops
70	31	49.2	45	5	ABP07880	Abp07880 Human ORF
71	31	49.2	50	5	AAV74355	Aav74355 Human col
72	31	49.2	53	4	ADR41394	Adr41394 Human CD-
73	31	49.2	53	5	ABB11899	Abb11899 Human HSP
74	31	49.2	54	4	AAW79411	Aaw79411 Human pro
75	31	49.2	54	4	AAW79410	Aaw79410 Human pro
76	31	49.2	54	6	ABO00908	Abos00908 Polypepti
77	31	49.2	54	6	ABO00764	Abos00764 Polypepti
78	31	49.2	54	6	AAU45795	Aau45795 Propionib
79	31	49.2	59	4	AAU45795	Aau45795 Propionib
80	31	49.2	59	6	ABM42314	Abm42314 Propionib
81	31	49.2	67	2	AAAR60622	Aaar60622 Pseudorab
82	31	49.2	70	4	AAV58694	Aav58694 Human EST
83	30	47.6	5	3	AAV58700	Aav58700 Antiangio
84	30	47.6	5	3	AAE00871	Aae00871 Leukocyte
85	30	47.6	15	4	ABB45085	Abb45085 Rat album
86	30	47.6	15	5	AAAB47985	Aaab47985 Human cyt
87	30	47.6	15	8	ADJ73696	Adj73696 Rat serum
88	30	47.6	19	7	ADE36966	Ade36966 Titanium
89	30	47.6	20	8	ADR05536	Adr05536 Novel ssp
90	30	47.6	22	7	ADE37042	Ade37042 Cell bind
91	30	47.6	23	6	ABOI2917	Aboi2917 Mouse zin
92	30	47.6	25	4	AAU06016	Aau06016 Cone snai
93	30	47.6	28	4	AAW16475	Aaw16475 Peptide #
94	30	47.6	28	8	ADK49312	Adk49312 Human car
95	30	47.6	35	4	ABB43193	Abb43193 Peptide #
96	30	47.6	35	4	AAW37033	Aaw37033 Peptide #
97	30	47.6	35	4	AAW76926	Aaw76926 Human bon
98	30	47.6	35	4	AAW76926	Aaw76926 Human bon

99 30 47.6 35 4 AAm64100 Human bra
100 30 47.6 35 4 ABg58588 Human liv

ALIGNMENTS

RESULT 1
AAV58691
ID AAV58691 standard; peptide; 11 AA.

XX AC AAY58691;
XX DT 25-APR-2000 (first entry)
XX DE Antiangiogenic peptide derived from saposin B.
XX KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
XX KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
XX OS Homo sapiens.
XX PN WO200002902-A1.
XX PD 20-JAN-2000.
XX PF 12-JUL-1999; 99WO-US015772.
XX PR 13-JUL-1998; 98US-0092647P.
XX PA (GILL/) GILL P S.
XX PI Gill PS;
XX DR WPI; 2000-171128/15.
XX PT Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.
XX PS Claim 23; Page 59; 78pp; English.

The present sequence is that of a claimed peptide, derived from human saposin B, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumour activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars

Sequence 11 AA;
Query Match 100.0%; Score 63; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GDVQCDCIQMV 11
DB 1 GDVQCDCIQMV 11

RESULT 2
AAV58693
ID AAV58693 standard; peptide; 10 AA.

XX AAY58693;
XX DT 25-APR-2000 (first entry)
XX DE Antiangiogenic peptide derived from saposin B.
XX KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
XX KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
XX OS Homo sapiens.
XX PN WO200002902-A1.
XX PD 20-JAN-2000.
XX PF 12-JUL-1999; 99WO-US015772.
XX PR 13-JUL-1998; 98US-0092647P.
XX PA (GILL/) GILL P S.
XX PI Gill PS;
XX DR WPI; 2000-171128/15.
XX PT Saposin B derived peptides, useful as inhibitors of angiogenesis and tumor growth.
XX PS Disclosure; Page 19; 78pp; English.
XX CC The present sequence is that of a novel peptide, derived from human saposin B, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumour activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars
XX SQ Sequence 10 AA;
Query Match 90.5%; Score 57; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DVCQDCIQMV 11
DB 1 DVCQDCIQMV 10
RESULT 3
AAV58685
ID AAV58685 standard; peptide; 15 AA.
XX AC AAY58685;
XX DT 25-APR-2000 (first entry)
XX DE Antiangiogenic peptide derived from saposin B.
XX KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
XX KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.

OS Synthetic.
 OS Homo sapiens.
 XX WO200002902-A1.
 XX PN
 XX 20-JAN-2000.
 XX PD
 XX 12-JUL-1999; 99WO-US015772.
 XX PF
 XX 13-JUL-1998; 98US-0092647P.
 XX PR
 XX (GILL/) GILL P S.
 XX PA
 XX Gill PS;
 XX PI
 XX WPI; 2000-171128/15.
 XX DR
 XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
 PT tumor growth.
 PT
 XX Disclosure; Page 19; 78pp; English.
 XX PS
 CC The present sequence is that of a novel peptide, based on a human saposin
 CC B derived peptide, that has antiangiogenic activity. The invention is
 CC based on the discovery that saposin B (see AAY58716), previously known to
 CC be involved in the hydrolysis of sphingolipids, has potent antiangiogenic
 CC and antitumor activity, and also has antiproliferative and antimigratory
 CC activity against endothelial cells. This activity is conserved in cryptic
 CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
 CC synthetically prepared and used in vitro or in vivo for the treatment of
 CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
 CC (claimed). The polypeptides can also be used in conjunction with
 CC cytotoxic moieties to selectively kill certain cell types, e.g. for
 CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
 CC malformation, nonunion fracture, arthritis and other connective tissue
 CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
 CC corneal graft neovascularization, pyogenic granuloma, retrolental
 CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
 CC vascular adhesions and hypertrophic scars
 XX Sequence 15 AA;
 SQ
 Query Match 87.3%; Score 55; DB 3; Length 15;
 Best Local Similarity 90.0%; Pred. No. 0.034;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GDVCDQCIQM 10
 DB 6 GDVCDQCIQV 15
 RESULT 4
 AAY58696
 ID AAY58696 standard; peptide; 9 AA.
 XX AC
 XX AAY58696;
 XX OS
 XX 25-APR-2000 (first entry)
 XX DT
 XX DE Antiangiogenic peptide derived from saposin B.
 XX KW
 XX Antiangiogenic; angiogenesis inhibitor; antitumor; antiproliferative;
 XX antiangiogenic; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX OS
 XX Homo sapiens.
 XX OS
 XX WO200002902-A1.
 XX PN
 XX 20-JAN-2000.
 XX PD
 XX 12-JUL-1999; 99WO-US015772.
 XX PF
 XX 13-JUL-1998; 98US-0092647P.
 XX PR

XX (GILL/) GILL P S.
 XX PI
 XX Gill PS;
 XX WPI; 2000-171128/15.
 XX DR
 XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
 PT tumor growth.
 PT
 XX Disclosure; Page 19; 78pp; English.
 XX PS
 CC The present sequence is that of a novel peptide, derived from human
 CC saposin B, that has antiangiogenic activity. The invention is based on
 CC the discovery that saposin B (see AAY58716), previously known to be
 CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
 CC and antitumor activity, and also has antiproliferative and antimigratory
 CC activity against endothelial cells. This activity is conserved in cryptic
 CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
 CC synthetically prepared and used in vitro or in vivo for the treatment of
 CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
 CC (claimed). The polypeptides can also be used in conjunction with
 CC cytotoxic moieties to selectively kill certain cell types, e.g. for
 CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
 CC malformation, nonunion fracture, arthritis and other connective tissue
 CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
 CC corneal graft neovascularization, pyogenic granuloma, retrolental
 CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
 CC vascular adhesions and hypertrophic scars
 XX Sequence 9 AA;
 SQ
 Query Match 84.1%; Score 53; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DVCQDCIQM 10
 DB 1 DVCQDCIQM 9
 RESULT 5
 AAY58704
 ID AAY58704 standard; peptide; 11 AA.
 XX AC
 XX AAY58704;
 XX OS
 XX 25-APR-2000 (first entry)
 XX DT
 XX DE Antiangiogenic peptide derived from saposin B.
 XX KW
 XX Antiangiogenic; angiogenesis inhibitor; antitumor; antiproliferative;
 XX antiangiogenic; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX OS
 XX Synthetic.
 XX OS
 XX Homo sapiens.
 XX OS
 XX WO200002902-A1.
 XX PN
 XX 20-JAN-2000.
 XX PD
 XX 12-JUL-1999; 99WO-US015772.
 XX PF
 XX 13-JUL-1998; 98US-0092647P.
 XX PR
 XX (GILL/) GILL P S.
 XX PA
 XX Gill PS;
 XX PI
 XX WPI; 2000-171128/15.
 XX DR
 XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
 PT tumor growth.
 PT

XX Disclosure; Page 19; 78pp; English.

XX The present sequence is that of a novel peptide, based on a human saposin B derived peptide, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumour activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars

XX Sequence 11 AA;

Query Match 84.1%; Score 53; DB 3; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.054;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GDVQCDCIQMV 11
| | | | | | | | | |
DB 1 GDVQCDCIQMV 11

RESULT 6

AAY58705

ID AAY58705 standard; peptide; 11 AA.

AC AAY58705;

DT 25-APR-2000 (first entry)

XX Antiangiogenic peptide derived from saposin B.

DE Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
KW Antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.

XX Synthetic.

OS Homo sapiens.

XX WO200002902-A1.

XX 20-JAN-2000.

XX 12-JUL-1999; 99WO-US015772.

XX 13-JUL-1998; 98US-0092647P.

XX (GILL/) GILL P S.

XX Gill PS;

XX WPI; 2000-171128/15.

XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
PT tumor growth.

XX Disclosure; Page 19; 78pp; English.

XX The present sequence is that of a novel peptide, based on a human saposin B derived peptide, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumour activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic

CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars

XX Sequence 11 AA;

Query Match 84.1%; Score 53; DB 3; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.054;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GDVQCDCIQMV 11
| | | | | | | | | |
DB 1 GDVQCDCIQMV 11

RESULT 7

AAY58701

ID AAY58701 standard; peptide; 9 AA.

AC AAY58701;

DT 25-APR-2000 (first entry)

XX Antiangiogenic peptide derived from saposin B.

XX Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
KW Antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.

XX Homo sapiens.

XX WO200002902-A1.

XX 20-JAN-2000.

XX 12-JUL-1999; 99WO-US015772.

XX 13-JUL-1998; 98US-0092647P.

XX (GILL/) GILL P S.

XX Gill PS;

XX WPI; 2000-171128/15.

XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
PT tumor growth.

XX Disclosure; Page 19; 78pp; English.

XX The present sequence is that of a novel peptide, derived from human saposin B, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumour activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,

CC vascular adhesions and hypertrophic scars

SQ Sequence 9 AA;

Query Match 81.0%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VCQDCIQMV 11

Db 1 VCQDCIQMV 9

RESULT 8

AAV58697
ID AAV58697 standard; peptide; 8 AA.

AC AAV58697;

DT 25-APR-2000 (first entry)

DE Antiangiogenic peptide derived from saposin B.

KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.

OS Homo sapiens.

PN WO200002902-A1.

PD 20-JAN-2000.

PF 12-JUL-1999; 99WO-US015772.

PR 13-JUL-1998; 98US-0092647P.

PA (GILL/) GILL P S.

PI Gill PS;

DR WPI; 2000-171128/15.

PT Saposin B derived peptides, useful as inhibitors of angiogenesis and
PT tumor growth.

PS Disclosure; Page 19; 78pp; English.

The present sequence is that of a novel peptide, derived from human saposin B, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumour activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars

SQ Sequence 8 AA;

Query Match 76.2%; Score 48; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DVCQDCIQ 9

|||||

Db 1 DVCQDCIQ 8

RESULT 9

AAV58702
ID AAV58702 standard; peptide; 8 AA.

AC AAY58702;

DT 25-APR-2000 (first entry)

DE Antiangiogenic peptide derived from saposin B.

KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.

OS Homo sapiens.

PN WO200002902-A1.

PD 20-JAN-2000.

PF 12-JUL-1999; 99WO-US015772.

PR 13-JUL-1998; 98US-0092647P.

PA (GILL/) GILL P S.

PI Gill PS;

DR WPI; 2000-171128/15.

PT Saposin B derived peptides, useful as inhibitors of angiogenesis and
PT tumor growth.

PS Disclosure; Page 19; 78pp; English.

The present sequence is that of a novel peptide, derived from human saposin B, that has antiangiogenic activity. The invention is based on the discovery that saposin B (see AAY58716), previously known to be involved in the hydrolysis of sphingolipids, has potent antiangiogenic and antitumour activity, and also has antiproliferative and antimigratory activity against endothelial cells. This activity is conserved in cryptic polypeptides as small as 5 amino acids (see AAY58684-715), which can be synthetically prepared and used in vitro or in vivo for the treatment of undesired angiogenesis and tumor growth, especially Kaposi's sarcoma (claimed). The polypeptides can also be used in conjunction with cytotoxic moieties to selectively kill certain cell types, e.g. for treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous malformation, nonunion fracture, arthritis and other connective tissue disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis, corneal graft neovascularization, pyogenic granuloma, retrolental fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma, vascular adhesions and hypertrophic scars

SQ Sequence 8 AA;

Query Match 74.6%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CQDCIQMV 11

Db 1 CQDCIQMV 8

RESULT 10

AAW18588
ID AAW18588 standard; peptide; 19 AA.

AC AAW18588;

DT 01-FEB-1998 (first entry)

XX Universal primary sperm-egg binding protein inactive fragment.
 XX
 KW Universal primary sperm-egg binding protein; UPSEBP; fertility;
 XX contraceptive.
 XX
 OS Synthetic.
 XX
 PN WO9725620-A1.
 XX
 PD 17-JUL-1997.
 XX
 PF 06-JAN-1997; 97WO-US000105.
 XX
 PR 11-JAN-1996; 96US-00584671.
 XX
 XX (PENN-) PENN STATE RES FOUND.
 XX
 PI Hammerstedt RH, Cramer PG, Barbato GF;
 XX
 XX WPI; 1997-373003/34.
 XX
 PT Protein providing for initial binding of sperm to oocyte investment(s) -
 PT used for enhancing sperm binding, contraception and determining the
 PT number of sperm binding sites on an oocyte investment.
 XX
 PS Disclosure; Page 29; 46pp; English.
 XX
 CC A synthetic peptide (see AAW18581) provides sperm binding capability
 CC similar to that of universal primary sperm-egg binding protein (UPSEBP).
 CC UPSEBP was originally isolated from rooster sperm. It provides for
 CC initial bonding of sperm to oocyte investments and has biological
 CC activity in a variety of avian and mammalian species. A shorter amino
 CC acid sequence (AAW18586) of the synthetic peptide is devoid of binding
 CC capability, and addition of amino acids distal to the N-terminal Aen
 CC residue of this short peptide (AAW18587 and AAW18588) did not
 CC substantially alter biological activity. Native or synthetic UPSEBPs can
 CC be used in claimed methods for enhancing sperm-egg binding, particularly
 CC of thawed cryopreserved sperm, for determining the fertilisation
 CC potential of sperm, and for determining the number of sperm binding
 CC binding sites on an egg investment. Analogues of the polypeptides that
 CC bind sperm but not oocytes can be used as contraceptives
 XX
 SQ Sequence 19 AA;
 Query Match 74.6%; Score 47; DB 2; Length 19;
 Best Local Similarity 70.0%; Pred. No. 0.86;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DVCQDCIQMV 11
 DB 8 DVCQDCMKLV 17
 |||||:::
 RESULT 11
 AAY58698
 ID AAY58698 standard; peptide; 7 AA.
 XX
 AC AAY58698;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Antiangiogenic peptide derived from saposin B.
 XX
 KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
 KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200002902-A1.
 XX
 PD 20-JAN-2000.
 XX

PF 12-JUL-1999; 99WO-US015772.
 XX
 PR 13-JUL-1998; 98US-0092647P.
 XX
 PA (GILL/) GILL P S.
 XX
 PI Gill PS;
 XX
 DR WPI; 2000-171128/15.
 XX
 PT Saposin B derived peptides, useful as inhibitors of angiogenesis and
 PT tumor growth.
 XX
 PS Disclosure; Page 19; 78pp; English.
 XX
 CC The present sequence is that of a novel peptide, derived from human
 CC saposin B, that has antiangiogenic activity. The invention is based on
 CC the discovery that saposin B (see AAY58716), previously known to be
 CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
 CC and antitumour activity, and also has antiproliferative and antimigratory
 CC activity against endothelial cells. This activity is conserved in cryptic
 CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
 CC synthetically prepared and used in vitro or in vivo for the treatment of
 CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
 CC (claimed). The polypeptides can also be used in conjunction with
 CC cytotoxic moieties to selectively kill certain cell types, e.g. for
 CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
 CC malformation, nonunion fracture, arthritis and other connective tissue
 CC disorders, Orlow-Weber syndrome, atherosclerotic plaque, psoriasis,
 CC corneal graft neovascularization, pyogenic granuloma, retrolental
 CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
 CC vascular adhesions and hypertrophic scars
 XX
 SQ Sequence 7 AA;
 Query Match 68.3%; Score 43; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DVCQDCI 8
 DB 1 DVCQDCI 7
 |||||
 RESULT 12
 AAY58692
 ID AAY58692 standard; peptide; 11 AA.
 XX
 AC AAY58692;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Antiangiogenic peptide derived from saposin B.
 XX
 KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
 KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO200002902-A1.
 XX
 PD 20-JAN-2000.
 XX
 PF 12-JUL-1999; 99WO-US015772.
 XX
 PR 13-JUL-1998; 98US-0092647P.
 XX
 PA (GILL/) GILL P S.
 XX
 PI Gill PS;
 XX
 DR WPI; 2000-171128/15.

XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
PT tumor growth.
XX
XX Disclosure; Page 19; 78pp; English.
XX
XX The present sequence is that of a novel peptide, based on a human saposin
CC B derived peptide, that has antiangiogenic activity. The invention is
CC based on the discovery that saposin B (see AAY58716), previously known to
CC be involved in the hydrolysis of sphingolipids, has potent antiangiogenic
CC and antitumor activity, and also has antiproliferative and antimigratory
CC activity against endothelial cells. This activity is conserved in cryptic
CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
CC synthetically prepared and used in vitro or in vivo for the treatment of
CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
CC (claimed). The polypeptides can also be used in conjunction with
CC cytotoxic moieties to selectively kill certain cell types, e.g. for
CC treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
CC malformation, nonunion fracture, arthritis and other connective tissue
CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
CC corneal graft neovascularization, pyogenic granuloma, retrolental
CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
CC vascular adhesions and hypertrophic scars
XX
XX Sequence 11 AA;
SQ

Query Match 68.3%; Score 43; DB 3; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GDVQDCIQMV 11
||| |||
DB 1 GDVQDSIQMV 11

RESULT 13
ADH32471
ID ADH32471 standard; protein; 60 AA.
XX
XX AC ADH32471;
XX
XX 11-MAR-2004 (first entry)
XX
XX Yeast smORF224-encoded polypeptide, SEQ ID NO:929.
DE
XX Open reading frame; ORF; identification; in silico; yeast; smORF;
KW small open reading frame; antisense therapy; antibody therapy;
KW drug screening; fungal infection; fungicide; gene therapy; vaccine.
XX
XX Saccharomyces cerevisiae.
OS
XX WO200268693-A2.
XX
XX 06-SEP-2002.
XX
XX 27-FEB-2002; 2002WO-US005677.
XX
XX 27-FEB-2001; 2001US-0271406P.
XX
XX 29-NOV-2001; 2001US-0333726P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Zeng Q, Kessler M, Cottarel G;
PI
XX WPI; 2002-707018/76.
XX
XX N-PSDB; ADH31798.
XX
XX Identifying open reading frames (ORFs) in a genome of an organism by
PT comparing genomic sequences to one or more genomic libraries containing
PT ORFs, useful for diagnosing, preventing and/or treating fungal
PT infections.
XX
XX Claim 38; SEQ ID NO 929; 160pp; English.
PS

XX The invention relates to a method of identifying open reading frames
CC (ORFs) in a genome of an organism. The method comprises: collecting a
CC genomic sequence of a first organism; comparing the genomic sequence of
CC the first organism to one or more other genomic libraries comprising
CC genomes of other organisms containing ORFs; and determining ORFs for the
CC first organism based on the comparison. The invention also relates to
CC smORFs (small open reading frames) from the Saccharomyces cerevisiae
CC genome which encode polypeptides less than 100 amino acids long; vectors
CC and host cells comprising a smORF; polypeptides encoded by the smORFs;
CC antisense compounds targeted to the smORFs and methods for their use in
CC inhibiting smORF expression; a method of identifying an inhibitor of a
CC smORF-encoded protein; an antibody against a smORF-encoded polypeptide;
CC and a composition comprising a smORF or smORF-encoded polypeptide and a
CC carrier. The invention provides a useful in silico method of identifying
CC new coding sequences, including homologues of coding sequences, in yeast
CC and other organisms. The compositions of the invention, and methods of
CC their use or discovery are also useful for diagnosing, preventing and/or
CC treating fungal infections. Sequences ADH32216-ADH32888 represent
CC specifically claimed yeast smORF-encoded polypeptides. Note: The sequence
CC data for this patent is not represented in the printed specification but
CC is based on sequence information supplied to Derwent by the European
CC Patent Office.
XX
XX Sequence 60 AA;
SQ

Query Match 65.1%; Score 41; DB 5; Length 60;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GDVQDCIQ 9
||| |||
DB 28 GDACSDFCQ 36

RESULT 14
AAW18587
ID AAW18587 standard; peptide; 15 AA.
XX
XX AC AAW18587;
XX
XX 01-FEB-1998 (first entry)
XX
XX Universal primary sperm-egg binding protein inactive fragment.
DE
XX Universal primary sperm-egg binding protein; UPSEBP; fertility;
KW contraceptive.
KW
XX Synthetic.
OS
XX WO9725620-A1.
XX
XX 17-JUL-1997.
XX
XX 06-JAN-1997; 97WO-US000105.
XX
XX 11-JAN-1996; 96US-00584671.
XX
XX (PENN-) PENN STATE RES FOUND.
XX
XX Hammerstedt RH, Cramer PG, Barbato GF;
PI
XX WPI; 1997-373003/34.
XX
XX Protein providing for initial binding of sperm to oocyte investment (s) -
PT used for enhancing sperm binding, contraception and determining the
PT number of sperm binding sites on an oocyte investment.
XX
XX Disclosure; Page 29; 46pp; English.
PS
XX A synthetic peptide (see AAW18581) provides sperm binding capability
CC similar to that of universal primary sperm-egg binding protein (UPSEBP).
CC UPSEBP was originally isolated from rooster sperm. It provides for
CC

CC initial bonding of sperm to oocyte investments and has biological
 CC activity in a variety of avian and mammalian species. A shorter amino
 CC acid sequence (AAW18586) of the synthetic peptide is devoid of binding
 CC capability, and addition of amino acids distal to the N-terminal Asn
 CC residue of this short peptide (AAW18587 and AAW18588) did not
 CC substantially alter biological activity. Native or synthetic UPSEBPs can
 CC be used in claimed methods for enhancing sperm-egg binding, particularly
 CC of thawed cryopreserved sperm, for determining the fertilisation
 CC potential of sperm, and for determining the number of sperm binding
 CC binding sites on an egg investment. Analogues of the polypeptides that
 CC bind sperm but not oocytes can be used as contraceptives

SQ Sequence 15 AA;
 Query Match 63.5%; Score 40; DB 2; Length 15;
 Best Local Similarity 85.7%; Pred. No. 9.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 1;

QY 2 DVCQDCI 8
 |||||:
 Db 9 DVCQDCM 15

RESULT 15
 ADE37012
 ID ADE37012 standard; peptide; 22 AA.
 XX AC ADE37012;
 XX DT 29-JAN-2004 (first entry)
 XX DE Binding agent related peptide SEQ ID NO:73.
 XX KW interfacial biomaterial; binding agent; biological substrate; cytostatic;
 XX KW Tie2 receptor antagonist; cell culture; biological array;
 KW transplant cell; transplant tissue; Tie2 receptor modulation;
 KW tumour angiogenesis.
 OS Synthetic.
 XX WO2003072542-A2.
 XX PD 04-SEP-2003.
 PF 20-NOV-2002; 2002WO-US037414.
 XX PR 20-NOV-2001; 2001US-0331843P.
 XX FA (UYDU-) UNIV DUKE.
 XX PI Grinstaff MW, Kenan DJ, Walsh EB, Middleton C;
 XX WPI; 2003-833266/77.
 DR New interfacial biomaterial having binding agents that binds a non-
 PT biological and biological substrate, useful in cell culture, in the
 PT preparation of biological arrays, and for diagnostic and therapeutic
 PT interface.
 XX Claim 90; SEQ ID NO 73; 150pp; English.

CC The present invention describes an interfacial biomaterial (I) comprising
 CC binding agents, each having a first ligand that specifically binds a
 CC target non-biological substrate and a second ligand that specifically
 CC binds a target biological substrate. The binding agents define an
 CC interface between the target non-biological substrate and the target
 CC biological substrate, or a non-binding domain substantially lacks binding
 CC to a target biological substrate. (I) has cytostatic activity, and can be
 CC used as a Tie2 receptor antagonist. The methods and compositions of the
 CC present invention can be used in cell culture of fibroblasts, endothelial
 CC cells, stem cells, embryonic and newborn tissue cells and osteoblasts, in
 CC the preparation of biological arrays, in the enhancement of an
 CC interaction between biological materials, for coating implants for in

CC vivo use, for coating donor transplant cells or tissues, for diagnostic
 CC and therapeutic interface, and for modulating Tie2 receptors in tumour
 CC angiogenesis. The present sequence is used in the exemplification of the
 CC present invention.

SQ Sequence 22 AA;
 Query Match 63.5%; Score 40; DB 7; Length 22;
 Best Local Similarity 54.5%; Pred. No. 14;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GDVCQDCIQMW 11
 |||||:
 Db 2 GDSCSDCLKSV 12

RESULT 16
 AAY58699
 ID AAY58699 standard; peptide; 6 AA.
 XX AC AAY58699;
 XX DT 25-APR-2000 (first entry)
 XX DE Antiangiogenic peptide derived from saposin B.
 XX KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
 KW antimigratory; Kaposi's sarcoma; tumour; human; saposin B; therapy.
 XX OS Homo sapiens.
 XX PN WO200002902-A1.
 XX PD 20-JAN-2000.
 XX PF 12-JUL-1999; 99WO-US015772.
 XX PR 13-JUL-1998; 98US-0092647P.
 XX PA (GILL/) GILL P S.
 XX PI Gill PS;
 XX WPI; 2000-171128/15.
 DR Saposin B derived peptides, useful as inhibitors of angiogenesis and
 PT tumor growth.
 XX PS Disclosure; Page 19; 78pp; English.

CC The present sequence is that of a novel peptide, derived from human
 CC saposin B, that has antiangiogenic activity. The invention is based on
 CC the discovery that saposin B (see AAY58716), previously known to be
 CC involved in the hydrolysis of sphingolipids, has potent antiangiogenic
 CC and antitumour activity, and also has antiproliferative and antimigratory
 CC activity against endothelial cells. This activity is conserved in cryptic
 CC polypeptides as small as 5 amino acids (see AAY58684-715), which can be
 CC synthetically prepared and used in vitro or in vivo for the treatment of
 CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
 CC (claimed). The polypeptides can also be used in conjunction with
 CC cytotoxic moieties to selectively kill certain cell types, e.g. for
 CC treatment of cancer, angiodioma, neovascular glaucoma, arteriovenous
 CC malformation, nonunion fracture, arthritis and other connective tissue
 CC disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
 CC corneal graft neovascularization, pyogenic granuloma, retrolental
 CC fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
 CC vascular adhesions and hypertrophic scars

SQ Sequence 6 AA;
 Query Match 61.9%; Score 39; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DVCQDC 7
 DB 1 DVCQDC 6

RESULT 17

AA58703
 ID AA58703 standard; peptide; 7 AA.

AC AA58703;

DT 25-APR-2000 (first entry)

DE Antiangiogenic peptide derived from saposin B.

KW Antiangiogenic; angiogenesis inhibitor; antitumour; antiproliferative;
 antimitigatory; Kaposi's sarcoma; tumour; human; saposin B; therapy.

XX Homo sapiens.

OS WO200002902-A1.

PN 20-JAN-2000.

PD 12-JUL-1999; 99WO-US015772.

PF 13-JUL-1998; 98US-0092647P.

PA (GILL/) GILL P S.

PI Gill PS;

XX WPI; 2000-171128/15.

PT Saposin B derived peptides, useful as inhibitors of angiogenesis and
 tumor growth.

PS Disclosure; Page 19; 78pp; English.

XX The present sequence is that of a novel peptide, derived from human
 saposin B, that has antiangiogenic activity. The invention is based on
 the discovery that saposin B (see AA58716), previously known to be
 involved in the hydrolysis of sphingolipids, has potent antiangiogenic
 and antitumour activity, and also has antiproliferative and antimigratory
 activity against endothelial cells. This activity is conserved in cryptic
 polypeptides as small as 5 amino acids (see AA58684-715), which can be
 synthetically prepared and used in vitro or in vivo for the treatment of
 undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
 (claimed). The polypeptides can also be used in conjunction with
 cytotoxic moieties to selectively kill certain cell types, e.g. for
 treatment of cancer, angiofibroma, neovascular glaucoma, arteriovenous
 malformation, nonunion fracture, arthritis and other connective tissue
 disorders, Osler-Weber syndrome, atherosclerotic plaque, psoriasis,
 corneal graft neovascularization, pyogenic granuloma, retrolental
 fibroplasia, diabetic retinopathy, scleroderma, haemangioma, trachoma,
 vascular adhesions and hypertrophic scars

XX Sequence 7 AA;

Query Match 60.3%; Score 38; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QDCIQMV 11
 DB 1 QDCIQMV 7

RESULT 18

AAU45013
 ID AAU45013 standard; protein; 53 AA.

XX

AC AAU45013;

DT 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #5909.

KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 dermatological; osteopathic; neuroprotectant.

OS Propionibacterium acnes.

PN WO200181581-A2.

PD 01-NOV-2001.

PF 20-APR-2001; 2001WO-US012865.

PR 21-APR-2000; 2000US-0199047P.

PR 02-JUN-2000; 2000US-0208841P.

PR 07-JUL-2000; 2000US-0216747P.

PA (CORI-) CORIXA CORP.

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

DR N-PSDB; AAS59524.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
 vaccinating against and diagnosing infections, especially useful for
 treating acne vulgaris.

PS Example 1; SEQ ID NO 6208; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 polypeptides. The proteins and their associated DNA sequences are used in
 the treatment, prevention and diagnosis of medical conditions caused by
 P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 P. acnes is also involved in infections of bone, joints and the central
 nervous system, however it is particularly involved in the inflammatory
 lesions associated with acne vulgaris. A method for detecting the
 presence or absence of P. acnes in a patient comprises contacting a
 sample with a binding agent that binds to the proteins of the invention
 and determining the amount of bound protein in the sample. The
 polypeptides may be used as antigens in the production of antibodies
 specific for P. acnes proteins. These antibodies can be used to
 downregulate expression and activity of P. acnes polypeptides and
 therefore treat P. acnes infections. The antibodies may also be used as
 diagnostic agents for determining P. acnes presence, for example, by
 enzyme linked immunosorbent assay (ELISA). Note: the sequence data for
 this patent did not form part of the printed specification, but was
 obtained in electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences

XX Sequence 53 AA;

Query Match 58.7%; Score 37; DB 4; Length 53;
 Best Local Similarity 62.5%; Pred. No. 95;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 DVCQDCIQ 9
 DB 39 DGCQDCVE 46

RESULT 19

ABM41532
 ID ABM41532 standard; protein; 53 AA.

XX

AC ABM41532;
 XX 20-OCT-2003 (first entry)
 XX Propionibacterium acnes predicted ORF-encoded polypeptide #6208.
 DE Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 XX immunostimulant; immune response; vaccine.
 XX Propionibacterium acnes.
 XX WO2003033515-A1.
 XX 24-APR-2003.
 XX 11-OCT-2002; 2002WO-US032727.
 XX 15-OCT-2001; 2001US-00978825.
 XX (CORI-) CORIXA CORP.
 XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallieve-Douglas J;
 XX WPI; 2003-381789/36.
 DR N-PSDB; ACF64453.
 XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX Example 1; SEQ ID NO 6208; 1481pp; English.
 XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide; a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 53 AA;
 SQ

Query Match 58.7%; Score 37; DB 6; Length 53;
 Best Local Similarity 62.5%; Pred. No. 95;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 DVCQDCIQ 9
 DB 39 DCCQDCVE 46

RESULT 20
 AAM40216
 ID AAM40216 standard; protein; 71 AA.
 XX AAM40216;
 AC AAM40216;
 XX 22-OCT-2001 (first entry)
 DT Human polypeptide SEQ ID NO 3361.
 DE
 XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX Homo sapiens.
 OS
 XX WO200153312-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 26-DEC-2000; 2000WO-US034263.
 PF
 XX 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang Y, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX WPI; 2001-442253/47.
 DR N-PSDB; AAI59372.
 XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 PT Example 5; SEQ ID NO 3361; 10078pp; English.
 XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with nootropic.
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX Sequence 71 AA;
 SQ
 Query Match 58.7%; Score 37; DB 4; Length 71;
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DVCQDCIQ 9
 :||:|:|:

Db 20 NVCKDCLQ 27

RESULT 21
AAB73737
ID AAB73737 standard; protein; 71 AA.

XX AAB73737;
AC AAB73737;
XX 12-SEP-2001 (first entry)
DT Ring finger protein 8.
DE
XX
XX Ring finger protein 8; human; recombinant production; malignant tumour;
KW cancer; blood disease; HIV infection; human immunodeficiency virus;
KW immune disorder; inflammatory condition; cytostatic; anti-HIV;
KW antiinflammatory; immunomodulator.
KW
XX Homo sapiens.
OS
XX WO200146243-A2.
PN
XX 28-JUN-2001.
PD
XX 11-DEC-2000; 2000WO-CN000544.
PF
XX 21-DEC-1999; 99CN-00125659.
PR
XX (UYFU-) UNIV FUDAN.
PA (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.
XX
XX Mao Y, Xie Y;
PI
XX WPI; 2001-418033/44.
DR N-PSDB; AAH25986.
XX
XX Ring finger protein 8 and encoded polynucleotide, applicable in diagnosis
PT and treatment of malignant neoplasm, hemopathy, HIV infection,
PT immunological diseases and inflammation.
XX
XX Claim 1; Page 30; 32pp; Chinese.
PS
XX This sequence represents ring finger protein 8. The protein has a
CC molecular weight of 8 kD, and has homology with a ring finger protein
CC given in AAB73739 over a 64 amino acid stretch. The invention relates to
CC ring finger protein 8 (AAB73737), nucleic acids encoding it (AAH25986),
CC and a method for the recombinant production of ring finger protein 8. The
CC present invention additionally discloses an agonist of ring finger
CC protein 8 for therapeutic use, and an antibody which specifically binds
CC to ring finger protein 8. Ring finger protein 8, and nucleotides which
CC encode it may be used for treating a variety of diseases, such as
CC malignant tumours, blood diseases, HIV (human immunodeficiency virus)
CC infection, immune disorders and inflammatory conditions. The protein may
CC also be used to screen for modulators of its activity or for peptide
CC fingerprinting identification. The polynucleotide can be used as a primer
CC for nucleic acid amplification reactions or as a probe for hybridisation
CC reactions, or in producing gene chips or microarrays
XX
SQ Sequence 71 AA;

Query Match 58.7%; Score 37; DB 4; Length 71;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 DVCDCICQ 9
DB 20 NVCKDCLQ 27

RESULT 22
AAO14371
ID AAO14371 standard; peptide; 31 AA.
XX

AC AAO14371;
XX
XX 24-MAY-2002 (first entry)
XX
XX Human metalloproteinase-like/disintegrin-like protein #15.
DE
XX Human; metalloproteinase-like/disintegrin-like protein; MPD;
KW angiogenesis; endothelial cell migration; integrin ligand binding;
KW ocular disorder; cancer; inflammation; osteoporosis; restenosis;
KW cytostatic; antiinflammatory; osteopathic; vasotropic; thrombolytic;
KW vulnary; antiallergic; antibacterial; virucide; protozoacide; cardiant;
KW antianaemic; analgesic; thrombosis; tissue repair; neural disorder;
KW infection.
XX
XX Homo sapiens.
OS
XX WO200210406-A2.
PN
XX 07-FEB-2002.
PD
XX 27-JUL-2001; 2001WO-US023734.
PF
XX 28-JUL-2000; 2000US-0221838P.
PR
XX (IMMV) IMMUNEX CORP.
PA
XX Dubose RF, Wiley SR, Black RA;
PI
XX WPI; 2002-195965/25.
XX
XX Novel purified human metalloproteinase-disintegrin polypeptide, useful
PT for treating ocular and inflammatory disorders, osteoporosis, cancer,
PT restenosis, thrombosis, and chronic pain conditions.
XX
XX Claim 1; Fig 1; 101pp; English.
PS
XX The present invention provides a number of human metalloproteinase-like
CC /disintegrin-like (MPD) proteins and their fragments. These can be used
CC to identify treatments for ocular disorders, malignant and metastatic
CC conditions, inflammatory diseases, osteoporosis and other conditions
CC mediated by accelerated bone resorption, restenosis, inappropriate
CC platelet activation, recruitment or aggregation, thrombosis, conditions
CC requiring tissue repair or wound healing, endothelial migration,
CC angiogenesis, allergies, reproductive, neurological and vascular
CC conditions, infections, cardiovascular disorders such as myocardial
CC infarction, chronic pain conditions, endocrine system disorders.
CC gastrointestinal system disorders, genitourinary system disorders,
CC anaemia and haematological disorders. The present sequence is a protein
CC of the invention
XX
XX Sequence 31 AA;

Query Match 57.1%; Score 36; DB 5; Length 31;
Best Local Similarity 71.4%; Pred. No. 85;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GDVCQDC 7
DB 24 GDCKDC 30

RESULT 23
AAO15618
ID AAO15618 standard; protein; 56 AA.
XX
XX AAO15618;
AC
XX
XX 12-OCT-2001 (first entry)
DT
XX
XX Peptide #2052 encoded by probe for measuring cervical gene expression.
DE
XX Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.

```
XX OS Homo sapiens.
XX XX WO200157278-A2.
XX PN 09-AUG-2001.
XX PD
XX PF
XX PI
XX XX 30-JAN-2001; 2001WO-US000670.
XX XX 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PF WPI; 2001-488901/53.
XX DR
XX XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human cervical epithelial cells.
XX XX Claim 27; SEQ ID NO 20444; 487pp; English.
XX PS
XX CC The present invention relates to human single exon nucleic acid probes
XX CC (SENP; see AA110068-AA128459). The present sequence is a peptide encoded
XX CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
XX CC can be used to produce a single exon microarray, which can be used for
XX CC measuring human gene expression in a sample derived from human cervical
XX CC epithelial cells. By measuring gene expression, the probes are therefore
XX CC useful in grading and/or staging of diseases of the cervix, notably
XX CC cervical cancer. Note: The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX XX Sequence 56 AA;
XX SQ
XX Query Match 55.6%; Score 35; DB 4; Length 56;
XX Best Local Similarity 71.4%; Pred. No. 2.1e+02;
XX Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 GDVQCDC 7
XX DB |||:|||
XX 25 GGVCEDC 31
XX
XX RESULT 24
XX ABB34623
XX ID ABB34623 standard; peptide; 56 AA.
XX AC ABB34623;
XX DT 04-FEB-2002 (first entry)
XX DE Peptide #2129 encoded by human foetal liver single exon probe.
XX XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX OS Homo sapiens.
XX XX WO200157277-A2.
XX PN
XX PD 09-AUG-2001.
XX PF
XX XX 30-JAN-2001; 2001WO-US000669.
XX PF
XX XX 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PF WPI; 2001-488901/53.
XX DR
XX XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human placenta.
XX XX Claim 27; SEQ ID NO 27258; 639pp + Sequence Listing; English.
XX PS
XX CC The invention relates to a single exon nucleic acid probe for measuring
XX CC human gene expression in a sample derived from human foetal liver. The
XX CC single exon nucleic acid probes may be used for predicting, measuring and
XX CC displaying gene expression in samples derived from human foetal liver. The
XX CC present sequence is a peptide encoded by a single exon nucleic acid probe
XX CC of the invention. Note: The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX XX Sequence 56 AA;
XX SQ
XX Query Match 55.6%; Score 35; DB 4; Length 56;
XX Best Local Similarity 71.4%; Pred. No. 2.1e+02;
XX Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 GDVQCDC 7
XX DB |||:|||
XX 25 GGVCEDC 31
XX
XX RESULT 25
XX AAM28116
XX ID AAM28116 standard; protein; 56 AA.
XX XX
XX AC AAM28116;
XX XX 17-OCT-2001 (first entry)
XX DT
XX DE Peptide #2153 encoded by probe for measuring placental gene expression.
XX DE Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder.
XX XX Homo sapiens.
XX OS
XX XX WO200157272-A2.
XX PN
XX PD 09-AUG-2001.
XX PF
XX PF 30-JAN-2001; 2001WO-US000663.
XX XX
XX XX 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PF WPI; 2001-488901/53.
XX DR
XX XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human placenta.
```

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XX PS Claim 27; SEQ ID NO 28385; 654pp; English.
XX CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX SQ Sequence 56 AA;
    Query Match      55.6%; Score 35; DB 4; Length 56;
    Best Local Similarity 71.4%; Pred. No. 2.1e+02;
    Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGVQCDC 7
   | | | | |
Db 25 GGVQCDC 31
Search completed: June 30, 2005, 11:52:54
Job time : 36.2346 secs

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This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2005, 11:37:42 ; Search time 8.14815 Seconds
(Without alignments)
100.776 Million cell updates/sec

Title: US-09-743-684A-19

Perfect score: 63

Sequence: 1 GDVQDCIQWV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 298299

Minimum DB seq length: 0

Maximum DB seq length: 71

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCITUS COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	100.0	11	4	US-09-352-548-19
2	57	90.5	10	4	US-09-352-548-21
3	57	90.5	16	4	US-09-352-548-48
4	55	87.3	15	4	US-09-352-548-13
5	53	84.1	9	4	US-09-352-548-24
6	53	84.1	11	4	US-09-352-548-32
7	53	84.1	11	4	US-09-352-548-33
8	51	81.0	9	4	US-09-352-548-29
9	48	76.2	8	4	US-09-352-548-25
10	47	74.6	8	4	US-09-352-548-30
11	47	74.6	19	2	US-08-584-671-5
12	47	74.6	19	3	US-09-027-376-5
13	47	74.6	19	3	US-09-094-192-5
14	43	68.3	7	4	US-09-352-548-26
15	43	68.3	11	4	US-09-352-548-20
16	40	63.5	15	2	US-08-584-671-4
17	40	63.5	15	3	US-09-027-376-4
18	40	63.5	15	3	US-09-094-192-4
19	39	61.9	6	4	US-09-352-548-27
20	39	61.9	16	4	US-09-352-548-55
21	38	60.3	7	4	US-09-352-548-31
22	35	55.6	52	4	US-09-621-976-6386
23	33	52.4	6	4	US-09-352-548-23
24	33	52.4	45	1	US-08-331-394-10
25	33	52.4	45	1	US-08-250-858-10
26	33	52.4	45	1	US-08-446-915-10
27	33	52.4	45	2	US-08-744-139-10

28	33	52.4	45	4	US-08-779-599-10	Sequence 10, Appl
29	33	52.4	45	5	PCT-US95-06639-10	Sequence 10, Appl
30	33	52.4	46	2	US-08-691-814B-16	Sequence 16, Appl
31	33	52.4	47	3	US-09-052-089A-14	Sequence 14, Appl
32	32	50.8	9	3	US-09-510-738A-38	Sequence 38, Appl
33	32	50.8	9	4	US-09-861-966-38	Sequence 38, Appl
34	32	50.8	9	4	US-09-919-048-38	Sequence 38, Appl
35	32	50.8	16	4	US-09-352-548-56	Sequence 56, Appl
36	32	50.8	16	4	US-09-352-548-57	Sequence 57, Appl
37	32	50.8	63	4	US-09-513-999C-5804	Sequence 5804, Ap
38	32	50.8	67	4	US-09-540-236-2949	Sequence 2949, Ap
39	31	49.2	16	4	US-09-352-548-58	Sequence 58, Appl
40	31	49.2	56	3	US-08-974-549A-127	Sequence 127, App
41	31	49.2	56	4	US-09-402-181B-127	Sequence 127, App
42	31	49.2	56	4	US-09-721-456-127	Sequence 127, App
43	31	49.2	67	1	US-07-945-283-5	Sequence 5, Appl
44	31	49.2	67	4	US-09-082-358B-46	Sequence 46, Appl
45	31	49.2	70	4	US-09-248-796A-24524	Sequence 24524, A
46	30	47.6	5	4	US-09-352-548-22	Sequence 22, Appl
47	30	47.6	5	4	US-09-352-548-28	Sequence 28, Appl
48	30	47.6	9	3	US-09-393-554-8	Sequence 8, Appl
49	30	47.6	16	4	US-09-352-548-47	Sequence 47, Appl
50	30	47.6	16	4	US-09-352-548-54	Sequence 54, Appl
51	30	47.6	16	4	US-09-352-548-59	Sequence 59, Appl
52	30	47.6	25	4	US-09-749-637A-340	Sequence 340, App
53	30	47.6	33	3	US-09-177-249-114	Sequence 114, App
54	30	47.6	33	4	US-09-812-283-114	Sequence 114, App
55	30	47.6	49	3	US-09-230-637-60	Sequence 60, Appl
56	30	47.6	69	1	US-07-945-283-6	Sequence 6, Appl
57	30	47.6	69	4	US-09-107-532A-6142	Sequence 6142, Ap
58	30	47.6	70	4	US-09-352-548-44	Sequence 44, Appl
59	30	47.6	70	4	US-09-352-548-45	Sequence 45, Appl
60	30	47.6	70	4	US-09-352-548-46	Sequence 46, Appl
61	30	47.6	70	4	US-09-352-548-49	Sequence 49, Appl
62	30	47.6	70	4	US-09-352-548-50	Sequence 50, Appl
63	30	47.6	70	4	US-09-352-548-51	Sequence 51, Appl
64	30	47.6	70	4	US-09-352-548-52	Sequence 52, Appl
65	30	47.6	70	4	US-09-352-548-53	Sequence 53, Appl
66	29	46.0	5	4	US-09-352-548-36	Sequence 36, Appl
67	29	46.0	10	1	US-08-482-880-27	Sequence 27, Appl
68	29	46.0	10	2	US-08-273-274-27	Sequence 27, Appl
69	29	46.0	10	2	US-08-475-041-27	Sequence 27, Appl
70	29	46.0	10	2	US-08-335-832-45	Sequence 45, Appl
71	29	46.0	10	2	US-08-484-773-27	Sequence 27, Appl
72	29	46.0	13	2	US-08-335-832-26	Sequence 26, Appl
73	29	46.0	13	2	US-08-335-832-27	Sequence 27, Appl
74	29	46.0	17	2	US-08-743-894B-40	Sequence 40, Appl
75	29	46.0	24	2	US-08-749-852-49	Sequence 49, Appl
76	29	46.0	32	3	US-09-324-455-17	Sequence 17, Appl
77	29	46.0	35	3	US-09-324-455-9	Sequence 9, Appl
78	29	46.0	35	3	US-09-324-455-10	Sequence 10, Appl
79	29	46.0	35	4	US-09-205-258-756	Sequence 756, App
80	29	46.0	42	1	US-08-050-319B-35	Sequence 35, Appl
81	29	46.0	42	3	US-08-465-982-35	Sequence 35, Appl
82	29	46.0	43	3	US-09-052-089A-11	Sequence 11, Appl
83	29	46.0	44	1	US-08-208-108-8	Sequence 8, Appl
84	29	46.0	46	2	US-08-511-485-32	Sequence 32, Appl
85	29	46.0	46	2	US-08-511-485-33	Sequence 33, Appl
86	29	46.0	46	4	US-09-201-936-32	Sequence 32, Appl
87	29	46.0	46	4	US-09-201-936-33	Sequence 33, Appl
88	29	46.0	46	4	US-09-011-356-32	Sequence 32, Appl
89	29	46.0	46	4	US-09-011-356-33	Sequence 33, Appl
90	29	46.0	46	4	US-09-201-932-32	Sequence 32, Appl
91	29	46.0	46	4	US-09-201-932-33	Sequence 33, Appl
92	29	46.0	52	3	US-08-569-749-11	Sequence 11, Appl
93	29	46.0	52	3	US-08-569-749-12	Sequence 12, Appl
94	29	46.0	52	4	US-09-689-366-11	Sequence 11, Appl
95	29	46.0	52	4	US-09-689-366-12	Sequence 12, Appl
96	29	46.0	52	5	PCT-US96-12860-11	Sequence 11, Appl
97	29	46.0	52	5	PCT-US96-12860-12	Sequence 12, Appl
98	29	46.0	53	4	US-09-732-210-1042	Sequence 1042, Ap
99	29	46.0	53	4	US-09-270-767-39363	Sequence 39363, A
100	29	46.0	53	4	US-09-270-767-34580	Sequence 34580, A

ALIGNMENTS

RESULT 1
US-09-352-548-19
; Sequence 19, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:G1-V11
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-19

Query Match 100.0%; Score 63; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDVQDCIQMV 11
||| ||||| |||||
Db 1 GDVQDCIQMV 11

RESULT 2
US-09-352-548-21
; Sequence 21, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-V11
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-21

Query Match 90.5%; Score 57; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DVCQDCIQMV 11
||| ||||| |||||
Db 1 DVCQDCIQMV 10

RESULT 3
US-09-352-548-48

; Sequence 48, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(6)
; OTHER INFORMATION: Xaa = any amino acid, Xaa at positions 1-6 may be
; OTHER INFORMATION: present or absent
US-09-352-548-48

Query Match 90.5%; Score 57; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DVCQDCIQMV 11
||| ||||| |||||
Db 7 DVCQDCIQMV 16

RESULT 4
US-09-352-548-13
; Sequence 13, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-angiogenic
; OTHER INFORMATION: polypeptide
US-09-352-548-13

Query Match 87.3%; Score 55; DB 4; Length 15;
Best Local Similarity 90.0%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDVQDCIQMV 10
||| ||||| |||||
Db 6 GDVQDCIQMV 15

RESULT 5
US-09-352-548-24
; Sequence 24, Application US/09352548
; Patent No. 6500431


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; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; EARLIER FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-M10
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-24

Query Match      84.1%; Score 53; DB 4; Length 9;
Best Local Similarity 100.0%; Pred.No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DVCQDCIQM 10
Db      1 DVCQDCIQM 9

RESULT 6
US-09-352-548-32
; Sequence 32, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; EARLIER FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:G1-(S4)-(S4)-V11
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-32

Query Match      84.1%; Score 53; DB 4; Length 11;
Best Local Similarity 90.9%; Pred.No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy      1 GDVCQDCIQMV 11
Db      1 GDVSDCIQMV 11

RESULT 7
US-09-352-548-33
; Sequence 33, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; EARLIER FILING DATE: 1999-07-12
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; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:G1-(S7)-V11
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-33

Query Match      84.1%; Score 53; DB 4; Length 11;
Best Local Similarity 90.9%; Pred.No. 0.018;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GDVCQDCIQMV 11
Db      1 GDVCQDSIQMV 11

RESULT 8
US-09-352-548-29
; Sequence 29, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; EARLIER FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:V3-V11
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-29

Query Match      81.0%; Score 51; DB 4; Length 9;
Best Local Similarity 100.0%; Pred.No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 VCQDCIQMV 11
Db      1 VCQDCIQMV 9

RESULT 9
US-09-352-548-25
; Sequence 25, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; EARLIER FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-Q9
US-09-352-548-25

Query Match          76.2%; Score 46; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DVCQDCIQ 9
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Db 1 DVCQDCIQ 8

RESULT 10
US-09-352-548-30
; Sequence 30, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: US 60/092,647
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:C4-V11
US-09-352-548-30

Query Match          74.6%; Score 47; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CQDCIQMV 11
   |||||
Db 1 CQDCIQMV 8

RESULT 11
US-08-584-671-5
; Sequence 5, Application US/08584671
; Patent No. 5910568
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESSEE: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:

US-09-743-684a-19.ra1
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Query Match 74.6%; Score 47; DB 3; Length 19;
Best Local Similarity 70.0%; Pred. No. 0.27;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 DVCQDCIQMV 11
DB 8 DVCQDCMKLV 17

RESULT 13
US-09-094-192-5
; Sequence 5, Application US/09094192
; Patent No. 6103483
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM TO EGG SURFACES AND PRO
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MONAHAN, THOMAS J
; REGISTRATION NUMBER: 29835
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 814-865-6277
; TELEFAX: 814-865-3591
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-09-094-192-5

Query Match 74.6%; Score 47; DB 3; Length 19;
Best Local Similarity 70.0%; Pred. No. 0.27;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 DVCQDCIQMV 11
DB 8 DVCQDCMKLV 17

RESULT 14
US-09-352-548-26
; Sequence 26, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; EARLIER FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:D2-18
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-26

Query Match 68.3%; Score 43; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DVCQDCI 8
DB 1 DVCQDCI 7

RESULT 15
US-09-352-548-20
; Sequence 20, Application US/09352548
; Patent No. 6500431
; GENERAL INFORMATION:
; APPLICANT: Gill, Parkash S.
; APPLICANT: Parkash S. Gill, M.D., Inc.
; TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
; FILE REFERENCE: 017986-000410US
; CURRENT APPLICATION NUMBER: US/09/352,548
; CURRENT FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:G1- (S4, S7)-VII
; OTHER INFORMATION: anti-angiogenic polypeptide
US-09-352-548-20

Query Match 68.3%; Score 43; DB 4; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.69;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 GDVSQDSIQMV 11

RESULT 16
US-08-584-671-4
; Sequence 4, Application US/08584671
; Patent No. 5910568
; GENERAL INFORMATION:
; APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,
; APPLICANT: CRAMER, PALMER
; TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
; TITLE OF INVENTION: TO EGG SURFACES AND PROCEDURES FOR USE OF THIS MOLECULE
; TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
; ADDRESS: STATE UNIVERSITY
; STREET: 113 TECHNOLOGY CENTER
; CITY: UNIVERSITY PARK
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 16802-7000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: NEC 286

OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,671
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONAHAN, THOMAS J
REGISTRATION NUMBER: 29835
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 814-865-6277
TELEFAX: 814-865-3591
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
US-08-584-671-4

Query Match 63.5%; Score 40; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DVCODCI 8
Db 9 DVCQDCM 15

RESULT 17
US-09-027-376-4
Sequence 4, Application US/09027376
Patent No. 6004586
GENERAL INFORMATION:
APPLICANT: HAMMERSTEDT, ROY H, BARBATO, GUY F,
APPLICANT: CRAMER, PALMER
TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM
TITLE OF INVENTION: TO ENHANCE OR DECREASE POTENTIAL FERTILITY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA
ADDRESS: STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,376
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,671
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MONAHAN, THOMAS J
REGISTRATION NUMBER: 29835
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 814-865-6277
TELEFAX: 814-865-3591
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE

TOPOLOGY: UNKNOWN
US-09-027-376-4

Query Match 63.5%; Score 40; DB 3; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DVCODCI 8
Db 9 DVCQDCM 15

RESULT 18
US-09-094-192-4
Sequence 4, Application US/09094192
Patent No. 6103483
GENERAL INFORMATION:
APPLICANT: HAMMERSTEDT, ROY H., BARBATO, GUY F.
APPLICANT: CRAMER, PALMER
TITLE OF INVENTION: MOLECULE INVOLVED IN BINDING OF SPERM TO EGG SURFACES AND PROC
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE PENNSYLVANIA STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 16802-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,192
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONAHAN, THOMAS J
REGISTRATION NUMBER: 29835
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 814-865-6277
TELEFAX: 814-865-3591
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
US-09-094-192-4

Query Match 63.5%; Score 40; DB 3; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DVCODCI 8
Db 9 DVCQDCM 15

RESULT 19
US-09-352-548-27
Sequence 27, Application US/09352548
Patent No. 6500431
GENERAL INFORMATION:
APPLICANT: Gill, Parkash S.
APPLICANT: Parkash S. Gill, M.D., Inc.
TITLE OF INVENTION: No. 6500431el Inhibitors of Angiogenesis and Tumor Growth
FILE REFERENCE: 017986-000410US
CURRENT APPLICATION NUMBER: US/09/352,548
FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: US 60/092,647

; EARLIER FILING DATE: 1998-07-13
 ; NUMBER OF SEQ ID NOS: 59
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 23
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:D6-V12
 ; OTHER INFORMATION: anti-angiogenic polypeptide
 US-09-352-548-23

Query Match 52.4%; Score 33; DB 4; Length 6;
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 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DCIQMV 11
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 Db 1 DCIQMV 6

RESULT 24
 US-08-331-394-10
 ; Sequence 10, Application US/08331394
 ; Patent No. 5670319
 ; GENERAL INFORMATION:
 ; APPLICANT: Goedel, David V.
 ; APPLICANT: Roths, Mike
 ; TITLE OF INVENTION: Tumor Necrosis Factor
 ; TITLE OF INVENTION: Receptor-Associated Factors
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/331,394
 ; FILING DATE:
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/250858
 ; FILING DATE: 27-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Ginger R.
 ; REGISTRATION NUMBER: 33,055
 ; REFERENCE/DOCKET NUMBER: 897P1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-3216
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 45 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 US-08-331-394-10

Query Match 52.4%; Score 33; DB 1; Length 45;
 Best Local Similarity 62.5%; Pred. No. 1e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CODCIQMV 11
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 Db 24 COECISQV 31

RESULT 25
 US-08-250-858-10
 ; Sequence 10, Application US/08250858
 ; Patent No. 5708142
 ; GENERAL INFORMATION:
 ; APPLICANT: Goedel, David V.
 ; APPLICANT: Roths, Mike
 ; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
 ; NUMBER OF SEQUENCES: 62
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/250,858
 ; FILING DATE: 27-May-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Ginger R.
 ; REGISTRATION NUMBER: 33,055
 ; REFERENCE/DOCKET NUMBER: 897.1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-3216
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 45 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 US-08-250-858-10

Query Match 52.4%; Score 33; DB 1; Length 45;
 Best Local Similarity 62.5%; Pred. No. 1e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CODCIQMV 11
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 Db 24 COECISQV 31

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 Job time : 10.1481 secs

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OM protein - protein search, using sw model

Run on: June 30, 2005, 11:49:03 ; Search time 28.3827 Seconds
(without alignments)
149.519 Million cell updates/sec

Title: US-09-743-684A-19

Perfect score: 63

Sequence: 1 GDVQDCIQMV 11

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Gapop 10.0 , Gapext 0.5

Searched: 1722976 seqs, 385795295 residues

Total number of hits satisfying chosen parameters: 616042

Minimum DB seq length: 0

Maximum DB seq length: 71

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	40	63.5	22	14	US-10-300-694A-73
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4	39	61.9	50	16	US-10-767-701-54814
5	37	58.7	59	16	US-10-425-115-229596
6	37	58.7	64	16	US-10-425-115-192735
7	36	57.1	20	17	US-10-690-276-716
8	36	57.1	31	15	US-10-343-251A-15
9	36	57.1	50	17	US-10-690-276-721
10	35	55.6	25	18	US-10-944-473-4
11	35	55.6	31	15	US-10-424-599-203524
12	35	55.6	35	16	US-10-437-963-103264
13	35	55.6	35	9	US-09-864-761-35331
14	35	55.6	35	15	US-10-424-599-215987
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16	33	52.4	34	14	US-10-262-525-24
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Sequence 35331, A
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Sequence 6, Appli
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Sequence 130971,
Sequence 110343,
Sequence 38, Appl
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Sequence 38, Appl
Sequence 25, Appl
Sequence 145029,
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Sequence 11093,
Sequence 229209,
Sequence 222657,
Sequence 247675,
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Sequence 221713,
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Sequence 337941,
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Sequence 293673,
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Sequence 340, App
Sequence 49046, A
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Sequence 45838, A
Sequence 25, Appl
Sequence 58648, A
Sequence 3, Appli

85 30 47.6 46 15 US-10-424-599-147828
86 30 47.6 48 15 US-10-424-599-167758
87 30 47.6 49 15 US-10-424-599-266164
88 30 47.6 51 16 US-10-437-963-129320
89 30 47.6 52 15 US-10-424-599-179998
90 30 47.6 55 9 US-09-864-761-37337
91 30 47.6 55 15 US-10-424-599-200550
92 30 47.6 56 15 US-10-424-599-227513
93 30 47.6 56 16 US-10-437-963-155853
94 30 47.6 56 16 US-10-437-963-181356
95 30 47.6 56 16 US-10-425-115-304594
96 30 47.6 56 16 US-10-425-115-355329
97 30 47.6 58 16 US-10-425-115-275198
98 30 47.6 59 16 US-10-437-963-197131
99 30 47.6 62 15 US-10-424-599-247511
100 30 47.6 62 15 US-10-424-599-257985

ALIGNMENTS

RESULT 1

US-10-083-357-929
; Sequence 929, Application US/10083357
; Publication No. US20030054370A1
; GENERAL INFORMATION:
; APPLICANT: Olandong Zeng et al.
; TITLE OF INVENTION: Systemic Discovery of New Genes
; FILE REFERENCE: 032796-090
; CURRENT APPLICATION NUMBER: US/10/083,357
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 1346
; SEQ ID NO 929
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-083-357-929

Query Match 65.1%; Score 41; DB 14; Length 60;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GDVQDCDCIQ 9
||| |||
Db 28 GDACSDCFQ 36

RESULT 2

US-10-300-694A-73
; Sequence 73, Application US/10300694A
; Publication No. US20030185870A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Grinstaff, Mark W.
; APPLICANT: Kenan, Daniel J.
; APPLICANT: Walsh, Elisabeth B.
; APPLICANT: Middleton, Crystan
; TITLE OF INVENTION: INTERFACIAL BIOMATERIALS
; FILE REFERENCE: 180/143/2
; CURRENT APPLICATION NUMBER: US/10/300,694A
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/331,843
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:

; OTHER INFORMATION: Cell-binding and titanium-binding dual specificity peptide 73
US-10-300-694A-73

Query Match 63.5%; Score 40; DB 14; Length 22;
Best Local Similarity 54.5%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GDVQDCDCIQMV 11
||| |||:
Db 2 GDSCSDCLKSV 12

RESULT 3

US-10-424-599-148377
; Sequence 148377, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 148377
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_105005C.1.pep
US-10-424-599-148377

Query Match 61.9%; Score 39; DB 15; Length 48;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GDVQDCDCIQM 10
||| |||
Db 12 GKVCYDCIVM 21

RESULT 4

US-10-767-701-54814
; Sequence 54814, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 54814
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 14593947.pep
US-10-767-701-54814

Query Match 61.9%; Score 39; DB 16; Length 59;
Best Local Similarity 71.4%; Pred. No. 47;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDVQDC 7
|||:
Db 9 GDMCEDC 15

RESULT 5

US-10-425-115-229596
; Sequence 229596, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 229596
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_140985C.1.pap
US-10-425-115-229596

Query Match 58.7%; Score 37; DB 16; Length 50;
Best Local Similarity 71.4%; Pred. No. 85;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GDVQCDC 7
|:|||||
Db 23 GHICQDC 29

RESULT 6

US-10-425-115-192735
; Sequence 192735, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 192735
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_107358C.1.pap
US-10-425-115-192735

Query Match 58.7%; Score 37; DB 16; Length 64;
Best Local Similarity 62.5%; Pred. No. 1.1e-02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GDVQCDCI 8
|||:|:
Db 2 GDACQSC 9

RESULT 7

US-10-690-276-716
; Sequence 716, Application US/10690276
; Publication No. US20050112118A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Incorporated
; APPLICANT: Cimbara, Daniel
; APPLICANT: Heichman, Karen
; APPLICANT: Bartel, Paul
; APPLICANT: Mauck, Kimberly

; APPLICANT: Bush, Angie
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFLAMMATORY DISORDERS
; FILE REFERENCE: 1834.01
; CURRENT APPLICATION NUMBER: US/10/690,276
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: 09/727,384
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/168,377
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 60/168,379
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 60/185,056
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 10/035,344
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,571
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 10/035,343
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,572
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 10/099,924
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,179
; PRIOR FILING DATE: 2001-03-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 728
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 716
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-690-276-716

Query Match 57.1%; Score 36; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDVQCQD 6
|||||
Db 15 GDVQCQD 20

RESULT 8

US-10-343-251A-15
; Sequence 15, Application US/10343251A
; Publication No. US20040091473A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Black, Roy A
; APPLICANT: Dubose, Robert F
; APPLICANT: Wiley, Steve R
; TITLE OF INVENTION: METALLOPROTEINASE-DISINTEGRIN POLYPEPTIDES AND METHODS OF MAKING
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 6120-US
; CURRENT APPLICATION NUMBER: US/10/343,251A
; CURRENT FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-251A-15

Query Match 57.1%; Score 36; DB 15; Length 31;
Best Local Similarity 71.4%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GDVQCDC 7
|||:|:
Db 24 GDCCKDC 30

```
RESULT 9
US-10-690-276-721
; Sequence 721, Application US/10690276
; Publication No. US20050112118A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Incorporated
; APPLICANT: Cimborra, Daniel
; APPLICANT: Heichman, Karen
; APPLICANT: Bartel, Paul
; APPLICANT: Mauck, Kimberly
; APPLICANT: Bush, Angie
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFLAMMATORY DISORDERS
; FILE REFERENCE: 1834.01
; CURRENT APPLICATION NUMBER: US/10/690,276
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: 09/727,384
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/168,377
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 60/168,379
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 60/185,056
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 10/035,344
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,571
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 10/035,343
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,572
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 10/099,924
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,179
; PRIOR FILING DATE: 2001-03-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 728
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 721
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-690-276-721

Query Match      57.1%; Score 36; DB 17; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 GDVCQD 6
      |||||
Db      45 GDVCQD 50

RESULT 10
US-10-944-473-4
; Sequence 4, Application US/10944473
; Publication No. US20050130892A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Thomason, Adam Read
; APPLICANT: Zhukovsky, Eugene Alexander
; APPLICANT: Chu, Seung Yup
; TITLE OF INVENTION: BAPF Variants and Methods Thereof
; FILE REFERENCE: A-72175-3
; CURRENT APPLICATION NUMBER: US/10/944,473
; CURRENT FILING DATE: 2004-09-16
; PRIOR APPLICATION NUMBER: US 60/585,264
; PRIOR FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US 10/794,751
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 60/528,104
; PRIOR FILING DATE: 2003-12-08
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; PRIOR APPLICATION NUMBER: US 60/523,880
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US 60/482,081
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US 60/452,707
; PRIOR FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-944-473-4

Query Match      55.6%; Score 35; DB 18; Length 25;
Best Local Similarity 55.6%; Pred. No. 93;
Matches      5; Conservative      3; Mismatches      1; Indels      0; Gaps      0;

Qy      3 VCQDCIQMV 11
      |||||
Db      9 VTQDCLQI 17

RESULT 11
US-10-424-599-203524
; Sequence 203524, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 203524
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_25808C.1.pep
US-10-424-599-203524

Query Match      55.6%; Score 35; DB 15; Length 31;
Best Local Similarity 36.4%; Pred. No. 1.1e+02;
Matches      4; Conservative      4; Mismatches      3; Indels      0; Gaps      0;

Qy      1 GDVCQDCIQMV 11
      |||||
Db      4 GQICVDCMSLM 14

RESULT 12
US-10-437-963-103264
; Sequence 103264, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
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; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 103264
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_100710C.1.pep
US-10-437-963-103264

Query Match 55.6%; Score 35; DB 16; Length 54;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VCQDCIQMW 11
:||||:|
Db 38 LCQDCLEDV 46

RESULT 13
US-09-864-761-35331
; Sequence 35331, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35331

; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005048.2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EST_HUMAN HIT: BF081244.1, EVALUATE 4.00e-17
; OTHER INFORMATION: SWISSPROT HIT: P15800, EVALUATE 6.00e-21
US-09-864-761-35331

Query Match 55.6%; Score 35; DB 9; Length 56;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GDVCQDC 7
|:|:|
Db 25 GGVCEDC 31

RESULT 14
US-10-424-599-215987
; Sequence 215987, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 215987
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_37066C.1.pep
US-10-424-599-215987

Query Match 55.6%; Score 35; DB 15; Length 57;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GDVCQDC 7
|:|:|
Db 4 GKVCEDC 10

RESULT 15
US-10-634-679A-6
; Sequence 6, Application US/10634679A
; Publication No. US20040192601A1
; GENERAL INFORMATION:
; APPLICANT: Corvera, Silvia
; APPLICANT: Lamdright, David
; TITLE OF INVENTION: LIPID BINDING MOLECULES AND METHODS OF
; FILE REFERENCE: USE
; CURRENT APPLICATION NUMBER: US/10/634,679A
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/400,619

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; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-634-679A-6

Query Match      55.6%; Score 35; DB 16; Length 68;
Best Local Similarity 55.6%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      3 VCDCIQMV 11
Db      59 VCKDCYQIM 67

RESULT 16
US-10-262-525-24
; Sequence 24, Application US/10262525
; Publication No. US20030138848A1
; GENERAL INFORMATION:
; APPLICANT: Moarefi, Iseail
; APPLICANT: Scheufler, Clemens
; APPLICANT: Hartl, Ulrich
; APPLICANT: Brinker, Achim
; TITLE OF INVENTION: 3D Structure of Polypeptides Containing
; TITLE OF INVENTION: a TPR-Structure Motif with Chaperone-Binding Function,
; TITLE OF INVENTION: Crystals Thereof and Compounds for Inhibition of Said
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: 2685-1-001
; CURRENT APPLICATION NUMBER: US/10/262,525
; CURRENT FILING DATE: 2002-03-30
; PRIOR APPLICATION NUMBER: PCT/EP01/03617
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: DE 10015748.3
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: DE 10018335.2
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-525-24

Query Match      52.4%; Score 33; DB 14; Length 34;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      4 QCDCIQM 10
Db      24 CCECIQL 30

RESULT 17
US-10-424-599-193911
; Sequence 193911, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 193911
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; LENGTH: 41
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_17127C.1.pep
US-10-424-599-193911

Query Match      52.4%; Score 33; DB 15; Length 41;
Best Local Similarity 83.3%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 DVCQDC 7
Db      33 DVCQDC 38

RESULT 18
US-10-283-500-10
; Sequence 10, Application US/10283500
; Publication No. US20030120043A1
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,500
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,599
; FILING DATE: 07-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P0897C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-283-500-10

Query Match      52.4%; Score 33; DB 14; Length 45;
Best Local Similarity 62.5%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      4 QCDCIQMV 11
Db      24 QCCEISQV 31

RESULT 19
US-10-425-115-343562
; Sequence 343562, Application US/10425115
; Publication No. US20040214272A1
```

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; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 343562
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_76491C.1.pap
US-10-425-115-343562

Query Match      52.4%; Score 33; DB 16; Length 50;
Best Local Similarity 57.1%; Pred. No. 3.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 CQDCIQM 10
         |::||::
Db      29 CEDCLEV 35

RESULT 20
US-10-425-115-338554
; Sequence 338554, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 338554
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_71928C.1.pap
US-10-425-115-338554

Query Match      52.4%; Score 33; DB 16; Length 55;
Best Local Similarity 62.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 CQDCIQMV 11
         |::||::
Db      18 CYDCLQSV 25

RESULT 21
US-10-437-963-130971
; Sequence 130971, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
```

```
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 130971
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_33082C.1.pap
US-10-437-963-130971

Query Match      52.4%; Score 33; DB 16; Length 61;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 CQDCIQ 9
         |::||:
Db      43 CEDCLQ 48

RESULT 22
US-10-437-963-110343
; Sequence 110343, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 110343
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_14415C.1.pap
US-10-437-963-110343

Query Match      52.4%; Score 33; DB 16; Length 64;
Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 VCQDCI 8
         |::||
Db      19 VCRDCI 24

RESULT 23
US-09-919-048-38
; Sequence 38, Application US/09919048
; Patent No. US20020150908A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/A/D/CIP
; CURRENT APPLICATION NUMBER: US/09/919,048
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/861,966
; PRIOR FILING DATE: 2001-05-21
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; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 38
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 145-153 of the hepsin protein
US-09-919-048-38

Query Match 50.8%; Score 32; DB 9; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VCQDC 7
:||||
Db 5 ICQDC 9

RESULT 24
US-10-102-283-38
; Sequence 38, Application US/10102283
; Publication No. US20030027181A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/A/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/102,283
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 09/919,048
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 190
; SEQ ID NO 38
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 145-153 of the hepsin protein
US-10-102-283-38

Query Match 50.8%; Score 32; DB 14; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VCQDC 7
:||||
Db 5 ICQDC 9

RESULT 25
US-10-135-795-38
; Sequence 38, Application US/10135795
; Publication No. US20030077618A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/A/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/135,795
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 10/102,283
; PRIOR FILING DATE: 2002-03-20
; NUMBER OF SEQ ID NOS: 191
; SEQ ID NO 38
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 145-153 of the hepsin protein
US-10-135-795-38

Query Match 50.8%; Score 32; DB 14; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VCQDC 7
:||||
Db 5 ICQDC 9

Search completed: June 30, 2005, 12:02:13
Job time : 30.3827 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2005, 11:38:12 ; Search time 6.24691 Seconds

(without alignments)
169.425 Million cell updates/sec

Title: US-09-743-684A-19

Perfect score: 63

Sequence: 1 GDVQDCIQMV 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 21350

Minimum DB seq length: 0

Maximum DB seq length: 71

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR 79:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	63.5	46	2	E69830
2	36	57.1	47	2	I48943
3	34	54.0	42	2	A82802
4	34	54.0	71	2	C83306
5	32	50.8	53	2	A31113
6	31	49.2	38	2	A60216
7	31	49.2	48	2	T07435
8	31	49.2	63	2	C69303
9	31	49.2	64	1	TIOAB
10	31	49.2	71	2	A59412
11	30	47.6	54	2	H82693
12	30	47.6	59	2	H81730
13	30	47.6	61	2	B96577
14	30	47.6	66	2	T47270
15	30	47.6	67	2	D83719
16	30	47.6	69	1	F70041
17	30	47.6	71	2	H83014
18	29	46.0	49	2	S33432
19	29	46.0	50	2	T38209
20	29	46.0	50	2	S53431
21	29	46.0	55	2	C39942
22	29	46.0	55	2	D39942
23	29	46.0	56	2	B39942
24	29	46.0	56	2	A96978
25	29	46.0	58	2	G36953
26	29	46.0	68	2	E69536
27	29	46.0	70	2	E72171
28	29	46.0	71	2	F72222
29	28.5	45.2	40	2	D44336

30	28	44.4	37	2	G82917	ribosomal protein
31	28	44.4	37	2	B49923	ribosomal protein
32	28	44.4	37	2	C64219	ribosomal protein
33	28	44.4	37	2	S62820	ribosomal protein
34	28	44.4	66	2	C81433	50S ribosomal prot
35	28	44.4	67	2	B69529	hypothetical prote
36	28	44.4	70	2	E83932	hypothetical prote
37	28	44.4	71	1	IHER1	high potential iro
38	28	44.4	71	2	AB0014	50S ribosomal prot
39	28	44.4	71	2	T08482	plasmid maintenanc
40	27	42.9	30	2	A27375	photosystem I iron
41	27	42.9	37	1	SDDVES	desulfurodoxin - D
42	27	42.9	37	2	C41933	mating pheromone E
43	27	42.9	40	2	H71330	hypothetical prote
44	27	42.9	45	2	D45731	gene 39.2 protein
45	27	42.9	46	2	C53613	plectonin XI - spi
46	27	42.9	52	1	A33173	rubredoxin [valida
47	27	42.9	53	1	R3MX14	ribosomal protein
48	27	42.9	53	2	H84319	hypothetical prote
49	27	42.9	55	1	FECLCB	ferredoxin 2[4Fe-4
50	27	42.9	55	1	FECLCT	ferredoxin 2[4Fe-4
51	27	42.9	55	1	FECLCU	ferredoxin 2[4Fe-4
52	27	42.9	55	1	FEQFR	ferredoxin 2[4Fe-4
53	27	42.9	55	2	H82976	rubredoxin PA5350
54	27	42.9	55	2	JX0144	ferredoxin - Clost
55	27	42.9	56	1	FECLCP	ferredoxin 2[4Fe-4
56	27	42.9	57	2	B82814	rubredoxin XF0379
57	27	42.9	59	1	FEDVIV	ferredoxin [4Fe-4S
58	27	42.9	59	1	FEDV2N	ferredoxin 2[4Fe-4
59	27	42.9	61	1	FECL2	ferredoxin 2[4Fe-4
60	27	42.9	63	1	IHQFT	high potential iro
61	27	42.9	63	1	FEDV2V	ferredoxin [4Fe-4S
62	27	42.9	64	2	D81321	hypothetical prote
63	27	42.9	65	2	D84355	DNA-directed RNA p
64	27	42.9	67	1	TIILF2	trypsin inhibitor
65	27	42.9	67	1	TIILF3	trypsin inhibitor
66	27	42.9	68	2	G37042	hypothetical prote
67	27	42.9	69	2	AG2197	hypothetical prote
68	27	42.9	70	1	B64091	ribosomal protein
69	27	42.9	70	1	R5EC31	ribosomal protein
70	27	42.9	70	2	G91236	50S ribosomal subu
71	27	42.9	70	2	G86083	50S ribosomal subu
72	27	42.9	71	2	S36783	dephosphin short f
73	26	41.3	7	2	AI2016	formylglycinamide
74	26	41.3	34	2	B82679	hypothetical prote
75	26	41.3	37	2	D90582	ribosomal protein
76	26	41.3	46	2	I48944	cellular disintegr
77	26	41.3	54	1	S23075	protein PMP-D1 - m
78	26	41.3	56	2	D90257	conserved hypothet
79	26	41.3	57	1	S73628	ribosomal protein
80	26	41.3	57	2	G82787	hypothetical prote
81	26	41.3	58	2	C69365	ferredoxin (fdx-5)
82	26	41.3	60	2	G69934	hypothetical prote
83	26	41.3	61	1	A30024	ferredoxin [3Fe-4S
84	26	41.3	61	1	FEDV3A	ferredoxin [3Fe-4S
85	26	41.3	64	1	FEDVIA	ferredoxin [4Fe-4S
86	26	41.3	64	2	S27525	sigma-F transcribe
87	26	41.3	65	2	B25103	ferredoxin 2[4Fe-4
88	26	41.3	65	2	B35405	ferredoxin 2[4Fe-4
89	26	41.3	66	2	B86648	hypothetical prote
90	26	41.3	66	2	T44533	hypothetical prote
91	26	41.3	66	2	AG1908	hypothetical prote
92	26	41.3	67	2	I54754	integrin beta 7 su
93	26	41.3	67	2	S33854	hypothetical prote
94	26	41.3	69	2	D90529	50S ribosomal prot
95	26	41.3	69	2	G69872	hypothetical prote
96	26	41.3	70	2	D97255	50S ribosomal prot
97	26	41.3	70	2	S75672	hypothetical prote
98	26	41.3	71	1	IHPC	high potential iro
99	26	41.3	71	2	D91050	hypothetical prote
100	25.5	40.5	48	2	I48948	cellular disintegr

ALIGNMENTS

RESULT 1
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hypotheical protein yhfH - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E69830
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertez
A.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Pritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
teich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
Y, M.; Ogawa, K.; Ogiwara, A.; Oudaga, B.; Park, S.H.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanton,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: E69830
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-46 <KUN>
A:Cross-references: UNIPROT:007606; GB:Z99109; GB:AL009126; NID:92633260; PIDN:CAB12863.
A:Experimental source: strain 168
C:Genetics:
A:Gene: yhfH

Query Match 63.5%; Score 40; DB 2; Length 46;
Best Local Similarity 50.0%; Pred. No. 5.6;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GDVQCDCIQM 10
|:|:|:|:|:|:
Db 34 GNICNDCKIV 43
RESULT 2
I48943
cellular disintegrin-related protein 16-2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 16-Aug-2004
C:Accession: I48943
R:Weskamp, G.; Blobel, C.P.
Proc. Natl. Acad. Sci. U.S.A. 91, 2748-2751, 1994
A:Title: A new family of cellular proteins related to snake venom disintegrins.
A:Reference number: A53476; MUID:94195820; PMID:8146185
A:Accession: I48943
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-47 <RES>
A:Cross-references: UNIPROT:061072; EMBL:U06145; NID:g487138; PIDN:AAA18424.1; PID:g4871
C:Superfamily: disintegrin homology

Query Match 57.1%; Score 36; DB 2; Length 47;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GDVQCDC 7
|||:|:|:
Db 27 GDCKKDC 33
RESULT 3
A82802
hypotheical protein XF0471 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: A82802
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: A82802
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-42 <SIM>
A:Cross-references: UNIPROT:Q9PG31; GB:AE003897; GB:AE003849; NID:g9105313; PIDN:AAF8328
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0471

Query Match 54.0%; Score 34; DB 2; Length 42;
Best Local Similarity 57.1%; Pred. No. 49;
Matches 8; Conservative 1; Mismatches 1; Indels 4; Gaps 1;
Qy 2 DVCCDPPLFCIQMV 11
|:|:|:|:|:|:
Db 13 DLCCDPPLFCIQMV 26
RESULT 4
CS3306
kleB protein - plasmid RK2
N:Alternate names: kcrA2 protein
C:Species: plasmid RK2
C>Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 08-Oct-1999
C:Accession: CS3306; S00971
R:Kornacki, J.A.; Chang, C.H.; Figurski, D.H.
J. Bacteriol. 175, 5078-5090, 1993
A:Title: kil-kor regulon of promiscuous plasmid RK2: structure, products, and regulation
A:Reference number: A53306; MUID:93352413; PMID:8349548
A:Accession: CS3306
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <KOR>
A:Cross-references: GB:L18919; NID:g400385; PIDN:AAA92766.1; PID:g400388
R:Thomas, C.M.; Ibbotson, J.P.; Wang, N.; Smith, C.A.; Tipping, R.; Loader, N.M.
Nucleic Acids Res. 15, 5345-5359, 1988
A:Title: Gene regulation on broad host range plasmid RK2: identification of three novel
A:Reference number: S00970; MUID:88262548; PMID:2838814
A:Accession: S00971
A:Molecule type: DNA
A:Residues: 1-71 <THO>
A:Cross-references: EMBL:X07248; NID:g41866; PIDN:CAA30234.1; PID:g41868
C:Genetics:
A:Gene: kleB; kcrA2
A:Genome: plasmid
C:Keywords: DNA binding

Query Match 54.0%; Score 34; DB 2; Length 71;
Best Local Similarity 62.5%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GDVQCDCI 8

Db 38 GGICGDCI 45

RESULT 5
AC3113
hypothetical protein Atu4527 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AC3113
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, M.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AC3113
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-53 <KUR>
A:Cross-references: UNIPROT:O8U7C2; GB:AE008689; PIDN:AAL45321.1; PID:G17743012; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu4527
A:Map position: linear chromosome

Query Match 50.8%; Score 32; DB 2; Length 53;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GNVQDCPI 8
|||:|:
Db 11 GNVTRDCM 18

RESULT 6
AG0216
hyperglycemic hormone homolog - American lobster (fragments)
N:Alternate names: peptide G-1
C:Species: Homarus americanus (American lobster)
C>Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 13-Sep-1998
C:Accession: AG0216
R:Pavloff, M.S.; Goy, M.F.
J. Neurochem. 55, 788-797, 1990
A:Title: Purification and chemical characterization of peptide G-1, an invertebrate neu
A:Reference number: AG0216; MUID:90347460; PMID:2384751
A:Accession: AG0216
A:Molecule type: protein
A:Residues: 1-38 <PAV>
A:Superfamily: hyperglycemic hormone
C:Keywords: hormone

Query Match 49.2%; Score 31; DB 2; Length 38;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VCQDCIQM 10
|||:|:
Db 9 VCEDCYNL 16

RESULT 7
T07435
hypothetical protein 48a and 48b - Japanese black pine chloroplast
C:Species: chloroplast Pinus thunbergiana (Japanese black pine)
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: T07435
R:Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Taudzuki, T.; Sugiyama, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A:Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome
A:Reference number: Z16030; MUID:95024047; PMID:7937893

A:Accession: T07435
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-48 <WAK>
A:Cross-references: UNIPROT:Q36908; EMBL:D17510; NID:G529643; PIDN:BAA04315.1; PID:G126225
A:Accession: T07506
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-48 <WAZ>
A:Cross-references: EMBL:D17510; NID:G529643; PIDN:BAA04315.1; PID:G1262596
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match 49.2%; Score 31; DB 2; Length 48;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 VCQDCI 8
|||:|:
Db 19 VCTDCI 24

RESULT 8
C69303
ferredoxin (fdx-4) homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 12-Jul-2004
C:Accession: C69303
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: C69303
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-63 <KLE>
A:Cross-references: UNIPROT:O29822; GB:AE001075; GB:AE000782; NID:G2689398; PIDN:AAB9081
F:4-60/Domain: ferredoxin 2[4fe-4S] homology <FER>

Query Match 49.2%; Score 31; DB 2; Length 63;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 DVCQDCIQMV 11
|||:|:
Db 40 DECQECSCV 49

RESULT 9
TIOAB
trypsin inhibitor (Bowman-Birk) - Job's tears
C:Species: Coix lachryma-jobi (Job's tears)
C>Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C:Accession: S00349
R:ARY, M.B.; Shewry, P.R.; Richardson, M.
FEBS Lett. 229, 111-118, 1988
A:Title: The amino acid sequence of a cereal Bowman-Birk type trypsin inhibitor from ser
A:Reference number: S00349; MUID:88152203; PMID:3162215
A:Accession: S00349
A:Molecule type: protein
A:Residues: 1-64 <ARY>
A:Cross-references: UNIPROT:P07679
C:Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C:Keywords: duplication; proteinase inhibitor
F:10-35/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F:36-59/Domain: Bowman-Birk inhibitor repeat homology #status atypical <BB2>
F:9-61,10-25,15-23,32-39,36-49/Disulfide bonds: #status predicted
F:17/Inhibitory site: Arg (trypsin) #status predicted

Query Match 49.2%; Score 31; DB 1; Length 64;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DVCQDC 7
| | | |
Db 34 DACKDC 39

RESULT 10
A59412
KGD-Bearing platelet-aggregation disintegrin (ussuristatin) 2 - Agkistrodon ussuriensis
C;Species: Agkistrodon ussuriensis
C;Date: 01-Mar-2002 #sequence_revision 01-Mar-2002 #text_change 09-Jul-2004
C;Accession: A59412
R;Iterada, S.
J. Biochem. 125, 31-35, 1999
A;Title: Ussuristatin 2, A Novel KGD-Bearing Disintegrin from Agkistrodon ussuriensis Ve
A;Reference number: A59412
A;Accession: A59412
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-71 <TER>
A;Cross-references: UNIPROT:Q7LZT4
C;Keywords: anticoagulant; integrin inhibitor; venom

Query Match 49.2%; Score 31; DB 2; Length 71;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GDVCQDC 7
| | | |
Db 32 GDCCQDC 38

RESULT 11
H82693
hypothetical protein XF1339 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: H82693
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: For a complete list of authors see reference number A59328 below
A;Accession: H82693
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-54 <SIM>
A;Cross-references: UNIPROT:Q9PDP0; GB:AE003966; GB:AE003849; NID:g9106327; PIDN:AAF8414
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Camargo, D.M.; Carreir, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuchino, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1339

Query Match 47.6%; Score 30; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GDVCQ 5
| | | |
Db 12 GDVCQ 16

RESULT 12
H81730
ribosomal protein L32 TC0195 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: H81730
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: H81730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-59 <TET>
A;Cross-references: UNIPROT:Q9PLB2; GB:AE002286; GB:AE002160; NID:g7190225; PIDN:AAF3906
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0195
C;Superfamily: Escherichia coli ribosomal protein L32

Query Match 47.6%; Score 30; DB 2; Length 59;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GDVCQDCIQM 10
| | | | |
Db 27 GAVCNCKQV 36

RESULT 13
B96577
probable RNA polymerase II, 28841-29486 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: B96577
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 815-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: B96577
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-61 <STO>
A;Cross-references: UNIPROT:Q9C8M4; GB:AE005173; NID:gi0645362; PIDN:AGC21482.1; GSPDB:G

Query Match 47.6%; Score 30; DB 2; Length 61;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Qy 1 GDV--CQDC 7
| | | | |
Db 33 GDVFQCRDC 41

RESULT 14

T47270
hypothetical protein copP [imported] - Helicobacter felis
C:Species: Helicobacter felis
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47270
R:Bayle, D.; Wangler, S.; Weitzenecker, T.; Steinhilber, W.; Volz, J.; Przybylski, M.; S
J. Bacteriol. 180, 317-329, 1998
A:Title: Properties of the P-type ATPases encoded by the copAP operons of Helicobacter P
A:Reference number: Z24437; MUID:98101471; PMID:9440521
A:Accession: T47270
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-66 <BA>
A:Cross-references: UNIPROT:O32620; EMBL:AJ001932; NID:G2660538; PIDN:CAA05105.1; PID:G2
A:Experimental source: strain ATCC 49179
C:Genetics:
A:Gene: copP
C:Superfamily: mercuric resistance operon regulatory protein; heavy-metal-associated hom
F:7-36/Domain: heavy-metal-associated homology <HMA>

Query Match 47.6%; Score 30; DB 2; Length 66;
Best Local Similarity 36.4%; Pred. No. 3.2e+02;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GDVQCDCIQMV 11
| | | | |
Db 9 GMTQCHCVDKI 19

RESULT 15
D83719
mercuric transport system (mercuric-binding protein) BH0556 [imported] - Bacillus halodu
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: D83719
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: D83719
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-67 <STO>
A:Cross-references: UNIPROT:Q9KFC8; GB:AP001508; GB:BA000004; NID:G10172890; PIDN:BA042
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0556
C:Superfamily: mercuric resistance operon regulatory protein; heavy-metal-associated hom

Query Match 47.6%; Score 30; DB 2; Length 67;
Best Local Similarity 45.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GDVQCDCIQMV 11
| | | | |
Db 9 GMSQCHCVKAV 19

RESULT 16
F70041
probable mercuric ion-binding protein yvgY - Bacillus subtilis
N:Alternate names: periplasmic mercuric ion-binding protein merP homolog
C:Species: Bacillus subtilis
C:Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 09-Jul-2004
C:Accession: F70041
R:Kunst, F.; Ogawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.F.; Enlian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptratr, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Banchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: F70041
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-69 <KUN>
A:Cross-references: UNIPROT:O32221; GB:Z99121; GB:AL009126; NID:G2635827; PIDN:CABL5356.
A:Experimental source: strain 168
C:Genetics:
A:Gene: yvgY
C:Superfamily: mercuric resistance operon regulatory protein; heavy-metal-associated hom
C:Keywords: metal binding
F:8-37/Domain: heavy-metal-associated homology <HMA>
F:13,16/Binding site: mercury (Cys) #status predicted

Query Match 47.6%; Score 30; DB 1; Length 69;
Best Local Similarity 45.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GDVQCDCIQMV 11
| | | | |
Db 10 GMSQCHCVKAV 20

RESULT 17
H83014
SOS ribosomal protein L31 PA5049 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: H83014
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83014
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <STO>
A:Cross-references: UNIPROT:Q9HUD0; GB:AE004918; GB:AE004091; NID:G9951336; PIDN:AAG0843
A:Experimental source: strain PA01
C:Genetics:
A:Gene: rpmB; PA5049
C:Superfamily: Escherichia coli ribosomal protein L31

Query Match 47.6%; Score 30; DB 2; Length 71;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DVCQDC 7
| | | | |
Db 35 DVCSEC 40

RESULT 18
S53432
echistatin gamma - saw-scaled viper
C:Species: Echis carinatus (saw-scaled viper)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 16-Aug-2004
C:Accession: S53432
R:Chen, Y.L.; Huang, T.F.; Chen, S.W.; Tsai, I.H.
Biochem. J. 305, 513-520, 1995
A:Title: Determination of the structure of two novel echistatin variants and comparison
A:Reference number: S53431; MUID:95134234; PMID:7832768
A:Accession: S53432
A:Status: preliminary

A:Molecule type: protein
A:Residues: 1-49 <CHE>
A:Cross-references: UNIPROT:Q7LZK0
C:Superfamily: disintegrin homology
F;24-26/Region: cell attachment (R-G-D) motif

Query Match 46.0%; Score 29; DB 2; Length 49;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GDVQCDC 7
| | | | |
Db 5 GPCCRDC 11

RESULT 19
T38209
probable metallothionein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38209
R;Grishchuk, K.; McIntosh, J.R.; Devlin, K.; Churcher, C.; Barrell, B.G.; Rajandream, M.
submitted to the EMBL Data Library, February 1996
A:Reference number: Z21778
A:Accession: T38209
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-50 <DEV>
A:Cross-references: UNIPROT:Q9UTC0; EMBL:Z69730; PIDN:CAB57404.1; GSPDB:GN00066; SPDB:SF
A:Experimental source: strain 972h-; cosmid c22h10
C:Genetics:
A:Gene: SPDB:SPAC22H10.13
A:Map position: 1

Query Match 46.0%; Score 29; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CQDC 7
| | | | |
Db 23 CQDC 26

RESULT 20
S53431
echistatin beta - saw-scaled viper
C:Species: Echis carinatus (saw-scaled viper)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 16-Aug-2004
C:Accession: S53431
R;Chen, Y.L.; Huang, T.F.; Chen, S.W.; Tsai, I.H.
Biochem. J. 305, 513-520, 1995
A:Title: Determination of the structure of two novel echistatin variants and comparison
A:Reference number: S53431; MUID:95134234; PMID:7832768
A:Accession: S53431
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-50 <CHE>
A:Cross-references: UNIPROT:Q7LZK1
C:Superfamily: disintegrin homology
F;1-42/Domain: disintegrin homology (fragment) <DIS>
F;24-26/Region: cell attachment (R-G-D) motif

Query Match 46.0%; Score 29; DB 2; Length 50;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GDVQCDC 7
| | | | |
Db 5 GPCCRDC 11

RESULT 21
C29942

developmental control protein Krox-6.1b(+) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: C29942
R;Chavrier, P.; Lemaire, P.; Revelant, O.; Bravo, R.; Charnay, P.
Mol. Cell. Biol. 8, 1319-1326, 1988
A:Title: Characterization of a mouse multigene family that encodes zinc finger structure
A:Reference number: A29942; MUID:88216608; PMID:2452975
A:Accession: C29942
A:Molecule type: DNA
A:Residues: 1-55 <CHA>
A:Cross-references: UNIPROT:P10752; EMBL:M20756; NID:g198612; PIDN:AAA39386.1; PID:g19861
C:Keywords: DNA binding; zinc finger

Query Match 46.0%; Score 29; DB 2; Length 55;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VCQDC 7
| | | | |
Db 9 VCQEC 13

RESULT 22
D29942
developmental control protein Krox-6.1b(-) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: D29942
R;Chavrier, P.; Lemaire, P.; Revelant, O.; Bravo, R.; Charnay, P.
Mol. Cell. Biol. 8, 1319-1326, 1988
A:Title: Characterization of a mouse multigene family that encodes zinc finger structure
A:Reference number: A29942; MUID:88216608; PMID:2452975
A:Accession: D29942
A:Molecule type: DNA
A:Residues: 1-55 <CHA>
A:Cross-references: UNIPROT:P10753; EMBL:M20757; NID:g198614; PIDN:AAA39387.1; PID:g1986
C:Keywords: DNA binding; zinc finger

Query Match 46.0%; Score 29; DB 2; Length 55;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VCQDC 7
| | | | |
Db 7 VCQEC 11

RESULT 23
B29942
developmental control protein Krox-6.1a - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: B29942
R;Chavrier, P.; Lemaire, P.; Revelant, O.; Bravo, R.; Charnay, P.
Mol. Cell. Biol. 8, 1319-1326, 1988
A:Title: Characterization of a mouse multigene family that encodes zinc finger structure
A:Reference number: A29942; MUID:88216608; PMID:2452975
A:Accession: B29942
A:Molecule type: DNA
A:Residues: 1-56 <CHA>
A:Cross-references: UNIPROT:P10751; GB:M20755; NID:g198610; PIDN:AAA39385.1; FID:g198611
C:Keywords: DNA binding; zinc finger

Query Match 46.0%; Score 29; DB 2; Length 56;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VCQDC 7
| | | | |
Db 8 VCQEC 12

RESULT 24

A96978
zinc finger domain [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: A96978
R:Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183; 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: A96978
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-56 <KOR>
A:Cross-references: UNIPROT:Q97LC7; GB:AE001437; PIDN:AAK78612.1; PID:g15023508; GSPDB:G
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0635

Query Match 46.0%; Score 29; DB 2; Length 56;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VQDC 7
||:||
Db 7 VCKDC 11

RESULT 25

G36953
hypothetical protein (acol_3' region) - Pelobacter carbinolicus
C:Species: Pelobacter carbinolicus
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 12-Jul-2004
C:Accession: G36953
R:Oppermann, F.B.; Steinbuechel, A.
J. Bacteriol. 176; 469-485, 1994
A:Title: Identification and molecular characterization of the aco genes encoding the Pel
A:Reference number: A36953; MUID:94117383; PMID:8110297
A:Accession: G36953
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-58 <OPP>
A:Cross-references: UNIPROT:Q51596; GB:U01100; NID:9434021; PIDN:AAA18920.1; PID:9434028

Query Match 46.0%; Score 29; DB 2; Length 58;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GDVCQDCI 8
|:|:
Db 15 GECIQDCV 22

Search completed: June 30, 2005, 11:54:50
Job time : 8.24691 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2005, 11:46:17 ; Search time 29.8765 Seconds
(without alignments)
188.538 Million cell updates/sec

Title: US-09-743-684A-19

Perfect score: 63

Sequence: 1 GDVQCDCIQMV 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 132411

Minimum DB seq length: 0

Maximum DB seq length: 71

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	63.5	46	2 O07606	007606 bacillus su
2	36	57.1	56	2 O42594	O42594 xenopus lae
3	35	55.6	48	1 R332_MYCGE	P56850 mycoplasma
4	35	55.6	48	1 R332_MYCPN	P56850 mycoplasma
5	34	54.0	39	2 O62V19	O62V19 bacillus li
6	34	54.0	42	2 O8PG31	O8PG31 xylella fas
7	34	54.0	71	1 K8B2_SCOLI	P13965 escherichia
8	33.5	53.2	59	2 O81K11	O81K11 bacillus an
9	33	52.4	35	2 Q7UV56	Q7UV56 rhodospirill
10	33	52.4	42	2 Q732A2	Q732A2 bacillus ce
11	33	52.4	42	2 O819L0	O819L0 bacillus ce
12	33	52.4	42	2 O81MR8	O81MR8 bacillus an
13	33	52.4	48	2 O84U25	O84U25 arabidopsis
14	33	52.4	52	2 Q65RJ4	Q65RJ4 manheimia
15	33	52.4	61	2 Q6FIT1	Q6FIT1 mesoplasma
16	32	50.8	44	2 Q7PTN7	Q7PTN7 anophelis g
17	32	50.8	45	2 O838H2	O838H2 enterococu
18	32	50.8	53	2 O8U7C2	O8U7C2 agrobacteri
19	32	50.8	54	2 Q6F228	Q6F228 mesoplasma
20	32	50.8	58	2 Q7QTG9	Q7QTG9 giardia lam
21	31	49.2	48	2 Q36908	Q36908 pinus thunb
22	31	49.2	50	2 Q64R23	Q64R23 bacteroides
23	31	49.2	59	2 O8FPK3	O8FPK3 leptospira
24	31	49.2	61	1 FER2_CHLTE	O8KZ7 chlorobium
25	31	49.2	61	2 Q73FC3	Q73FC3 treponema d
26	31	49.2	62	2 Q7Y4U0	Q7Y4U0 bacterioph
27	31	49.2	62	2 Q7WZP9	Q7WZP9 candidatus
28	31	49.2	63	2 O29822	O29822 archaeoglob
29	31	49.2	64	1 IB81_COILA	P07679 coix lachry
30	31	49.2	65	2 O85X16	O85X16 pinus korai
31	31	49.2	67	2 Q6D8V8	Q6D8V8 erwinia car

32	31	49.2	71	1 DIS2_AKCA	Q71zt4 agkistrodon
33	31	49.2	71	2 Q7MQW3	Q7mqw3 wolinnella s
34	30.5	48.4	58	1 TX20_PHORI	P84031 phoneutria s
35	30.5	48.4	66	2 Q6KGS9	Q6kgs9 bacterioph
36	30	47.6	32	2 Q72HE5	Q72he5 thermus the
37	30	47.6	37	1 ME22_EUPRA	P58548 euplotus ra
38	30	47.6	37	2 Q6T3W6	Q6t3w6 heliconius
39	30	47.6	41	2 Q81XX5	Q81xx5 bacillus an
40	30	47.6	43	2 Q8ERX5	Q8erx5 oceanobacill
41	30	47.6	50	1 HUNB_PSYCI	Q02032 psychoda ci
42	30	47.6	54	2 Q9ZND7	Q9znd7 thermus the
43	30	47.6	54	2 Q9PDP0	Q9pdp0 xylella fas
44	30	47.6	56	2 Q848H0	Q848h0 uncultured
45	30	47.6	58	1 RL32_CHLMU	Q9p1b2 chlamydia m
46	30	47.6	61	2 Q9C8M4	Q9c8m4 arabidopsis
47	30	47.6	62	2 Q49267	Q49267 mycoplasma
48	30	47.6	63	2 Q855B9	Q855b9 mycobacteri
49	30	47.6	63	2 Q8NQJ8	Q8nqj8 corynebacte
50	30	47.6	66	1 COPP_HELPF	O36220 helicobacte
51	30	47.6	67	2 Q01676	Q01676 pneumocysti
52	30	47.6	67	2 Q9SRU5	Q9srus arabidopsis
53	30	47.6	67	2 Q9KFC8	Q9kfc8 bacillus ha
54	30	47.6	68	2 Q8VBV2	Q8vbv2 rattus norv
55	30	47.6	69	1 COP2_BACSU	O32221 bacillus su
56	30	47.6	69	2 Q8NEI9	Q8nei9 corynebacte
57	30	47.6	69	2 Q8K4N2	Q8k4n2 mus musculu
58	30	47.6	71	1 RL31_PSEAE	Q9hud0 pseudomonas
59	30	47.6	71	2 Q8WSH9	Q8wsh9 trachypenae
60	30	47.6	71	2 Q8WSI1	Q8wsi1 litopenaeus
61	30	47.6	71	2 Q8WSI2	Q8wsi2 eriocheir s
62	29	46.0	24	2 Q13660	Q13660 homo sapien
63	29	46.0	29	2 Q88227	Q88227 mus musculu
64	29	46.0	33	2 Q95P77	Q95p77 carcinus ma
65	29	46.0	35	2 Q7QTX3	Q7qtx3 giardia lam
66	29	46.0	38	2 Q65Y23	Q65y23 equus cabal
67	29	46.0	39	2 Q6TMT7	Q6tmt7 streptomyce
68	29	46.0	42	1 SEK1_CENEX	Q86ql centruroides
69	29	46.0	42	1 SEK1_CENLL	Q86qv0 centruroides
70	29	46.0	42	1 SEK1_CENSC	Q86gu6 centruroides
71	29	46.0	43	1 SEK5_CENNO	Q86p80 centruroides
72	29	46.0	43	2 Q95P80	Q95p80 carcinus ma
73	29	46.0	43	2 Q9GSZ0	Q9gsz0 carcinus ma
74	29	46.0	49	2 Q43697	Q43697 homo sapien
75	29	46.0	49	2 Q7LZK0	Q7lzk0 echis carin
76	29	46.0	50	2 Q9UTC0	Q9utc0 schizosacch
77	29	46.0	50	2 Q7LZK1	Q7lzk1 echis carin
78	29	46.0	51	2 Q6YTZ8	Q6ytz8 oryza sativ
79	29	46.0	51	2 Q8XMP2	Q8xmp2 clostridium
80	29	46.0	52	2 Q97894	Q97894 human immun
81	29	46.0	53	1 RL40_TETPY	P33190 tetrahymena
82	29	46.0	53	2 Q6Q0K8	Q6qok8 sulfolobus
83	29	46.0	54	2 Q95P76	Q95p76 carcinus ma
84	29	46.0	55	1 KRXB_MOUSE	P10752 mus musculu
85	29	46.0	55	1 KXKC_MOUSE	P10753 mus musculu
86	29	46.0	55	2 Q64A27	Q64a27 uncultured
87	29	46.0	55	2 Q64CE4	Q64ce4 uncultured
88	29	46.0	56	2 Q95P79	Q95p79 carcinus ma
89	29	46.0	56	1 KRXA_MOUSE	P10751 mus musculu
90	29	46.0	56	1 RL40_SULTO	Q976i5 sulfolobus
91	29	46.0	56	2 Q9HHD7	Q9hhd7 halobacteri
92	29	46.0	56	2 Q97LC7	Q97lc7 clostridium
93	29	46.0	58	2 Q51596	Q51596 pelobacter
94	29	46.0	59	2 Q7Y5D2	Q7y5d2 bacterioph
95	29	46.0	60	2 Q95P74	Q95p74 carcinus ma
96	29	46.0	60	2 Q95P75	Q95p75 carcinus ma
97	29	46.0	60	2 Q95P78	Q95p78 carcinus ma
98	29	46.0	60	2 Q7UEN0	Q7uen0 rhodopirell
99	29	46.0	60	2 Q7VDJ7	Q7vdj7 prochloroco
100	29	46.0	60	2 Q883A4	Q883a4 pseudomonas

ALIGNMENTS

DT	01-JAN-1998	(TEMBLrel. 05, Created)
DT	01-JAN-1998	(TEMBLrel. 05, Last sequence update)
DT	01-MAR-2004	(TEMBLrel. 26, Last annotation update)
DE	Metalloprotease/disintegrin xMDC13 (Fragment).	
OS	Xenopus laevis	(African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;	
OC	Xenopodinae; Xenopus.	
OX	NCBI_TaxID=8355;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Testis;	
RC	MEDLINE=97349132; PubMed=9205136; DOI=10.1006/dbio.1997.8586;	
RA	Shilling F.N., Kraetzschmar J., Cai H., Weskamp G., Gayko U.,	
RA	Leibow J., Myles D.G., Nuccitelli R., Blobel C.P.;	
RT	"Identification of metalloprotease/disintegrins in Xenopus laevis	
RT	testis with a potential role in fertilization."	
RL	Dev. Biol. 186:155-164(1997).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Testis;	
RA	Kraetzschmar J., Cai H., Blobel C.P.;	
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; U78186; AAB87146.1; -.	
DR	HSP; P21859; IJ2L.	
DR	MEROFS; M12.213; -.	
DR	GO; GO:0008237; F-metallopeptidase activity; IEA.	
DR	GO; GO:0007229; P-integrin-mediated signaling pathway; IEA.	
DR	InterPro; IPR001762; Disintegrin.	
DR	Pfam; PF00200; Disintegrin; 1.	
DR	ProDom; PD000664; Disintegrin; 1.	
DR	SMART; SM00050; DISIN; 1.	
DR	PROSITE; PS50214; DISINTEGRIN 2; 1.	
KW	Integrin; Metalloprotease; Protease.	
FT	NON_TER 1	
FT	NON_TER 56	
SQ	SEQUENCE 56 AA; 5861 MW; C375DF6C57CD883 CRC64;	
Query Match 57.1%; Score 36; DB 2; Length 56;		
Best Local Similarity 71.4%; Pred.No. 1.2e+02;		
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		
QY	1 GDVCQDC 7	
DB	1:	
	35 GECCQDC 41	
RESULT 3		
R332 MYCGE		
ID_R332 MYCGE STANDARD; PRT; 48 AA.		
AC Q3ZB52;		
DT 30-MAY-2000 (Rel. 39, Created)		
DT 30-MAY-2000 (Rel. 39, Last sequence update)		
DT 25-OCT-2004 (Rel. 45, Last annotation update)		
GN 50S ribosomal protein L33 type 2.		
DN Name=rpmc2; OrderedLocusNames=MG055.1;		
OS Mycoplasma genitalium.		
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.		
OC NCBI_TaxID=2097;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN=ATCC 33530 / G-37;		
EX MEDLINE=96026346; PubMed=7569993;		
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,		
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G.G., Kelley J.M.,		
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,		
RA Nguyen D.T., Uutterback T.B., Saudek D.M., Phillips C.A., Merrick J.M.,		
RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,		
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;		
RL "The minimal gene complement of Mycoplasma genitalium";		
RL Science 270:397-403(1995).		
RN [2]		
RP IDENTIFICATION.		

RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Uterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C., Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ribosomal protein L33P family.
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CC EMBL: U39684; AAC71272.1; -.
DR TIGR; MG055.1; -.
DR HAMAP; MF_00294; -; 1.
DR InterPro; IPR001705; Ribosomal L33.
DR ProDom; PD002595; Ribosomal L33; 1.
DR TIGRPFAMs; TIGR01023; rplM; 1.
DR PROSITE; PS00582; RIBOSOMAL_L33; FALSE_NEG.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 48 AA; 5946 MW; 33C7A47A3B98B65F CRC64;

Query Match 55.6%; Score 35; DB 1; Length 48;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VCQDCI 8
Db 8 VCQDCL 13
|||||

RESULT 4
R332 MYCPN STANDARD; PRT; 48 AA.
AC P56850;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S0S ribosomal protein L33 type 2.
GN Name=rpmG2; OrderedLocusNames=MPN069; ORFNames=MP085.1;
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RA MEDLINE=97105885; PubMed=8948633; DOI=10.1093/nar/24.22.4420;
RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C., Hermann R.;
RA "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae";
RT Nucleic Acids Res. 24:4420-4449 (1996).
RL -!- SIMILARITY: Belongs to the ribosomal protein L33P family.
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CC EMBL; AE000010; AAG34736.1; -.
DR HAMAP; MF_00294; -; 1.
DR InterPro; IPR001705; Ribosomal L33.
DR ProDom; PD002595; Ribosomal L33; 1.
DR TIGRPFAMs; TIGR01023; rplM; 1.
DR PROSITE; PS00582; RIBOSOMAL_L33; FALSE_NEG.

KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 48 AA; 5863 MW; 93A1A3157098ABED CRC64;

Query Match 55.6%; Score 35; DB 1; Length 48;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VCQDCI 8
Db 8 VCQDCL 13
|||||

RESULT 5
Q62VI9 PRELIMINARY; PRT; 39 AA.
AC Q62VI9;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=BL01620;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J., Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B., Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D., Berka R.M.;
RA "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species.";
RT Genome Biol. 5:R77-R77(2004).
RL EMBL; CP000002; AAU23219.1; -.
KW Hypothetical protein.
SQ SEQUENCE 39 AA; 4463 MW; CEDD838CD4055625 CRC64;

Query Match 54.0%; Score 34; DB 2; Length 39;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VCQDCIQMV 11
Db 5 VCQDCNETI 13
|||||

RESULT 6
Q9PG31 PRELIMINARY; PRT; 42 AA.
AC Q9PG31;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Xf0471;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OX Xanthomonadaceae; Xylella.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9asc;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvares R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H., Pacincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

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RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins A.L., Martins E.M.F., Matsukuma A.Y.,
RA Meek C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuchioka M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003897; AAF83281.1; -.
DR FIC; AB2802; AB2802.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 42 AA; 4690 MW; AAF5B1F2FA8E6DC9 CRC64;

Query Match 54.0%; Score 34; DB 2; Length 42;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

Qy 2 DVCQD----CIQMV 11
Db 13 DLCCDPPLFCIQMV 26

RESULT 7
KEB2_ECOLI STANDARD; PRT; 71 AA.
AC Q13955;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE KleB protein (KcrA2 protein).
GN Name=kleB; Synonyms=kcrA2;
OS Escherichia coli.
OG Plasmid IncP-alpha RK2.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=88262548; PubMed=2838814;
RA Thomas C.M., Ibbotson J.P., Wang N., Smith C.A., Tipping R.,
RA Loader N.M.;
RT "Gene regulation on broad host range plasmid RK2: identification of
RT three novel operons whose transcription is repressed by both KcrA and
RT KcrC.";
RL Nucleic Acids Res. 16:5345-5359(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=93352413; PubMed=8349548;
RA Kornacki J.A., Chang C.-H., Figureki D.H.;
RA "kil-kor regulon of promiscuous plasmid RK2: structure, products, and
RT regulation of two operons that constitute the kilE locus.";
RL J. Bacteriol. 175:5078-5090(1993).
CC -----
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CC -----
DR EMBL; X07248; CAA30234.1; -.
DR EMBL; L18919; AAA92766.1; -.
KW DNA-binding; Plasmid; Transcription regulation.
FT DNA BIND 9 28 H-T-H motif (By similarity).
SQ SEQUENCE 71 AA; 7605 MW; BDD9D998ABDAE04C CRC64;

Query Match 54.0%; Score 34; DB 1; Length 71;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GDVQCDCI 8
Db 38 GGICGDCI 45

RESULT 8
Q81K11 PRELIMINARY; PRT; 59 AA.
ID Q81K11 PRELIMINARY; PRT; 59 AA.
AC Q81K11; O6K188;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
DE OrderedLocusNames=BA5016, GBAA5016;
GN OrderedLocusNames=BA5016, GBAA5016;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Beanan M.J., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate 0581;
RX Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017039; AAP28696.1; -.
DR EMBL; AE017334; AAT34143.1; -.
DR TIGR; BA5016; -.
DR TIGR; GBAA5016; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 59 AA; 6870 MW; 0159182CC760CC61 CRC64;

Query Match 53.2%; Score 33.5; DB 2; Length 59;
Best Local Similarity 58.3%; Pred. No. 3.3e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 GDV-CQDCIQMV 11
Db 44 GEVYCSCIQIV 55

RESULT 9
Q7UV56 PRELIMINARY; PRT; 35 AA.
ID Q7UV56 PRELIMINARY; PRT; 35 AA.
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AC Q7UV56;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DE 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RB2863;
OS Rhodospirillum rubrum;
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=1117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RA MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Glueckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX2941137; CAD72870.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 35 AA; 4166 MW; B3C7A54B78AD800D CRC64;

Query Match 52.4%; Score 33; DB 2; Length 35;
Best Local Similarity 54.5%; Pred. No. 2.5e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GDVQCDCIQMV 11
Db 21 GDVNRRCIELV 31

RESULT 10
ID Q732A2 PRELIMINARY; PRT; 42 AA.
AC Q732A2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BCE4013;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Ockstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolatse A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017277; AAS42915.1; -.
DR TIGR; BCE4013; -.
KW Complete proteome.
SQ SEQUENCE 42 AA; 4546 MW; 1FA3D3DF18288E58 CRC64;

Query Match 52.4%; Score 33; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VCQDC 7
Db 5 VCQDC 9

RESULT 11
ID Q819L0 PRELIMINARY; PRT; 42 AA.
AC Q819L0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BC3966;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Gallon N., Candelon B.,
RA Kapral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fomstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017011; AAP10886.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 42 AA; 4546 MW; 1FA3D3DF18288E58 CRC64;

Query Match 52.4%; Score 33; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VCQDC 7
Db 5 VCQDC 9

RESULT 12
ID Q81MR8 PRELIMINARY; PRT; 42 AA.
AC Q81MR8; O6KNE5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BA4176; GBAA4176;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate Porton;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Ockstad O.A., Helgason E., Rinkstone J., Wu M.,
RA Kolonay J.F., Beaman M.J., Dodson R.J., Rinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaiter J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolatse A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL EMBL; AE017037; AAP27900.1; -.
DR EMBL; AE017334; AAT33298.1; -.
DR TIGR; BA4176; -.
DR TIGR; GBAA4176; -.

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KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 42 AA; 4546 MW; 1FA3D3DF18288E58 CRC64;

Query Match 52.4%; Score 33; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VCQDC 7
| | | | |
Db 5 VCQDC 9

RESULT 13
ID Q84U25 PRELIMINARY; PRT; 48 AA.
AC Q84U25;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein At5g45660.
GN Name=At5g45660;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsie.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yanada K., Chan M.M., Chang C.H., Dale J.M., Heuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shim P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT005028; AA050561.1; -.
DR InterPro; IPR000886; ER target S.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 48 AA; 5231 MW; A852B8EF05A111AC CRC64;

Query Match 52.4%; Score 33; DB 2; Length 48;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 GDVQDCIQM 10
| : | | | : :
Db 9 GELLQDCLEV 18

RESULT 14
ID Q6SRJ4 PRELIMINARY; PRT; 52 AA.
AC Q6SRJ4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MS1809;
OS Mannheimia succiniciproducens MBEL55E.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MBEL55E;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.-G., Kim J.G.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens.";
RL Nat. Biotechnol. 0:0-0(2004).
DR EMBL; AE016827; AAU38416.1; -.

KW Hypothetical protein.
SQ SEQUENCE 52 AA; 6304 MW; 4226E560A266FC2D CRC64;

Query Match 52.4%; Score 33; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VCQDC 7
| | | | |
Db 48 VCQDC 52

RESULT 15
ID Q6FIT1 PRELIMINARY; PRT; 61 AA.
AC Q6FIT1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Mf1185;
OS Mesoplasma florum (Acholeplasma florum).
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Entomoplasmataceae; Mesoplasma.
OX NCBI_TaxID=2151;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LI / ATCC 33453;
RA Birren B.W., Stange-Thomann N., Hafez N., DeCaprio D., Fisher S.,
RA Butler J., Elkins T., Kodira C.D., Major J., Wang S., Nicol R.,
RA Nusbaum C.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017263; AA075542.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 61 AA; 7055 MW; 0FD9A5AA3A87035 CRC64;

Query Match 52.4%; Score 33; DB 2; Length 61;
Best Local Similarity 62.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 QDCIQMV 11
| | | | |
Db 45 CHDCMQTV 52

RESULT 16
ID Q7PTN7 PRELIMINARY; PRT; 44 AA.
AC Q7PTN7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP00000018679.
GN Name=ENSANGP0000000016190;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
DR EMBL; AAAB01008797; EAA03618.2; -.
SQ SEQUENCE 44 AA; 4761 MW; 8C9F6FEEF5D40AC7 CRC64;

Query Match 50.8%; Score 32; DB 2; Length 44;
Best Local Similarity 44.4%; Pred. No. 4.5e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY      3 VCQDCIQMV 11
DB      17 ICSECMQSV 25

RESULT 17
Q838H2  PRELIMINARY;      PRT;      45 AA.
AC Q838H2;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=EF0477;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umavam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
RA Frazer C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis."
RL Science 299:2071-2074(2003).
DR EMBL; AE016948; AA080331.1; -.
DR TIGR; EF0477; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 45 AA; 4562 MW; 92289BD9BB5C5762 CRC64;

Query Match      50.8%; Score 32; DB 2; Length 45;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GDVQCDC 7
DB      25 GSECDCC 31

RESULT 18
Q8U7C2  PRELIMINARY;      PRT;      53 AA.
AC Q8U7C2;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein Atu4527.
GN OrderedLocusNames=Atu4527;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dupont;
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens

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RT C58.";
RL Science 294:2317-2323(2001).
DR EMBL; AE009381; AAL45321.1; -.
DR PIR; AC3113; AC3113.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR PRINTS; PR00939; C2HCZNFINGER.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 53 AA; 5585 MW; E8F0B4DBCC4AF119 CRC64;

Query Match      50.8%; Score 32; DB 2; Length 53;
Best Local Similarity 62.5%; Pred. No. 5.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GDVQCDCI 8
DB      11 GDVTRDCM 18

RESULT 19
Q6F228  PRELIMINARY;      PRT;      54 AA.
AC Q6F228;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE 50S ribosomal protein L33.
GN OrderedLocusNames=Mfl089;
OS Mesoplasma florum (Acholeplasma florum).
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Entomoplasmataceae; Mesoplasma.
OX NCBI_TaxID=2151;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L1 / ATCC 33453;
RA Birren B.W., Stange-Thomann N., Hafez N., DeCaprio D., Fisher S.,
RA Butler J., Elkins T., Kodira C.D., Major J., Wang S., Nicol R.,
RA Nusbaum C.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the L33P family of ribosomal proteins.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0006735; P:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR01705; Ribosomal L33.
DR Pfam; PF00471; Ribosomal L33; 1.
DR ProDom; PD002595; Ribosomal L33; 1.
DR TIGRPFMs; TIGR01023; rpmG_bact; 1.
KW Complete proteome; Ribonucleoprotein; Ribosomal protein.
SQ SEQUENCE 54 AA; 6468 MW; 987C7F16FCA5334A CRC64;

Query Match      50.8%; Score 32; DB 2; Length 54;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 VCQDCI 8
DB      13 VCEDCL 18

RESULT 20
Q7QTG9  PRELIMINARY;      PRT;      58 AA.
AC Q7QTG9;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE GLP 251 28892 29068.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Alley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000105; EAA38340.1; -.
SQ SEQUENCE 58 AA; 6372 MW; B2FBE6BDFB50439 CRC64;

Query Match 50.8%; Score 32; DB 2; Length 58;
Best Local Similarity 57.1%; Pred. No. 5.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VCQDCIQ 9
Db 26 VCSDCVR 32

RESULT 21
ID Q36908 PRELIMINARY; PRT; 48 AA.
AC Q36908;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE ORF48a (ORF48b)
OS Pinus thunbergii (Green pine) (Japanese black pine).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=33350;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92212283; PubMed=1557027;
RA Tsudzuki J., Nakashima K., Tsudzuki T., Hiratsuka J., Shibata M.,
RA Wakasugi T., Sugitara M.;
RT "Chloroplast DNA of black pine retains a residual inverted repeat
RT lacking rRNA genes: nucleotide sequences of trnQ, trnK, psbA, trnI and
RT trnH and the absence of rps16.";
RL Mol. Gen. Genet. 232:206-214(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95094312; PubMed=8001170;
RA Tsudzuki J., Ito S., Tsudzuki T., Wakasugi T., Sugitara M.;
RT "A new gene encoding tRNA pro (GGG) is present in the chloroplast
RT genome of black pine: a compilation of 32 tRNA genes from black pine
RT chloroplasts.";
RL Curr. Genet. 26:153-158(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95024047; PubMed=7937893;
RA Wakasugi T., Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,
RA Sugitara M.;
RT "Loss of all ndh genes as determined by sequencing the entire
RT chloroplast genome of the black pine pinus thunbergii.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:9794-9798(1994).
DR EMBL; D17510; BAA04315.1; -.
DR EMBL; D17510; BAA04384.1; -.
DR PIR; T07435; T07435.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
SQ SEQUENCE 48 AA; 5469 MW; DE9394D399008EB2 CRC64;

Query Match 49.2%; Score 31; DB 2; Length 48;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VCQDCI 8
Db 19 VCTDCI 24

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RESULT 22
Q64RZ3
ID Q64RZ3 PRELIMINARY; PRT; 50 AA.
AC Q64RZ3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=BP2990;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
DR EMBL; AP006841; BAD49738.1; -.
KW Hypothetical protein.
SQ SEQUENCE 50 AA; 5917 MW; CC2EA755BAA67EB9 CRC64;

Query Match 49.2%; Score 31; DB 2; Length 50;
Best Local Similarity 45.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GDVQCDCIQMV 11
Db 31 GSVCHRCILHTV 41

RESULT 23
Q8F9K3
ID Q8F9K3 PRELIMINARY; PRT; 59 AA.
AC Q8F9K3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=LA0192;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=1173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AE011209; AAN47391.1; -.
KW Complete proteome.
SQ SEQUENCE 59 AA; 6679 MW; EA8E2BC7D246E0A6 CRC64;

Query Match 49.2%; Score 31; DB 2; Length 59;
Best Local Similarity 42.9%; Pred. No. 8.6e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DVCQDCI 8
Db 19 DVCCECL 25

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RESULT 24
FER2_CHLITE STANDARD; PRT; 61 AA.
ID Q8KCZ7;
AC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ferredoxin II.
GN OrderedLocusNames=CT1260;
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobaculum.
OK NCBI_taxid=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TLS / ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,
RA Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,
RA Parksey D.S., Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B.,
RA Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,
RA Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
CC -!- FUNCTION: Ferredoxins are iron-sulfur proteins that transfer
CC electrons in a wide variety of metabolic reactions.
CC -!- COPACTOR: Binds 2 4Fe-4S clusters.
CC -!- SIMILARITY: Contains 2 4Fe-4S type ferredoxin domains.
CC -----
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CC -----
DR EMBL; AE012886; AAM72490.1; -;
DR HSP; P00198; 2FDN.
DR TIGR; CT1260; -;
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; Fer4; 1.
DR PRINTS; PR00353; 4FB4SPRD0XIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW 4Fe-4S; Complete proteome; Electron transport; Iron-sulfur; Repeat.
FT INIT_MET 0 0 By similarity.
FT METAL 8 8 Iron-sulfur 1 (4Fe-4S) (By similarity).
FT METAL 11 11 Iron-sulfur 1 (4Fe-4S) (By similarity).
FT METAL 14 14 Iron-sulfur 1 (4Fe-4S) (By similarity).
FT METAL 18 18 Iron-sulfur 2 (4Fe-4S) (By similarity).
FT METAL 37 37 Iron-sulfur 2 (4Fe-4S) (By similarity).
FT METAL 40 40 Iron-sulfur 2 (4Fe-4S) (By similarity).
FT METAL 49 49 Iron-sulfur 2 (4Fe-4S) (By similarity).
FT METAL 53 53 Iron-sulfur 1 (4Fe-4S) (By similarity).
SQ SEQUENCE 61 AA; 6493 MW; 63D8C8C2EC75E1C5 CRC64;

Query Match 49.2%; Score 31; DB 1; Length 61;
Best Local Similarity 71.4%; Pred. No. 8.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DVCQDCI 8
Db 35 NVCDVCI 41

RESULT 25
Q73PC3 PRELIMINARY; PRT; 61 AA.
ID Q73PC3
AC Q73PC3;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TDE0876;
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OK NCBI_taxid=158;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35405 / DSM 14222;
RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
RA Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
DR EMBL; AE017248; AAS11367.1; -;
DR TIGR; TDE0876; -;
DR InterPro; IPR010982; Lambda_like_DNA.
KW Complete proteome.
SQ SEQUENCE 61 AA; 7068 MW; 3777A66F83CDF71D CRC64;

Query Match 49.2%; Score 31; DB 2; Length 61;
Best Local Similarity 62.5%; Pred. No. 8.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GDVQDCI 8
Db 4 GSIQDFI 11

Search completed: June 30, 2005, 11:58:39
Job time : 33.8765 secs

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